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**FIG. 1**

<i>Bet v 1</i> sense	5' - AATTATGAGACTGAGACCA <u>C</u> CTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCTGGTGGAGACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACCC <u>C</u> CTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCTGGGGGAGACA	-5'



FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGCATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

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FIG. 3

1 (A-C)

GGTGTGTTTAATTATGAGACTGAGACCACTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60
G V F N Y E T E T T P S V I P A A R L F K 20

9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAGGTTGCACCCCAAGCCATTAGCAGT 120
A F I L D G G D N T L F P K Q V A P Q A I S S 40

3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)

GTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAGAAGATCAGCTTTCCCGAA 180
V E N I E S G N S G G P G T I K K N I S F P E S 60

5 (CA-TG)

GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAAACTTCAAA 240
G L P F K Y V K D R V D E V D H T A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC 300
Y N Y S V I E G G P I G D T L E K I S N 100

10 (GAG-CAC) 8 (CCC-TGG)

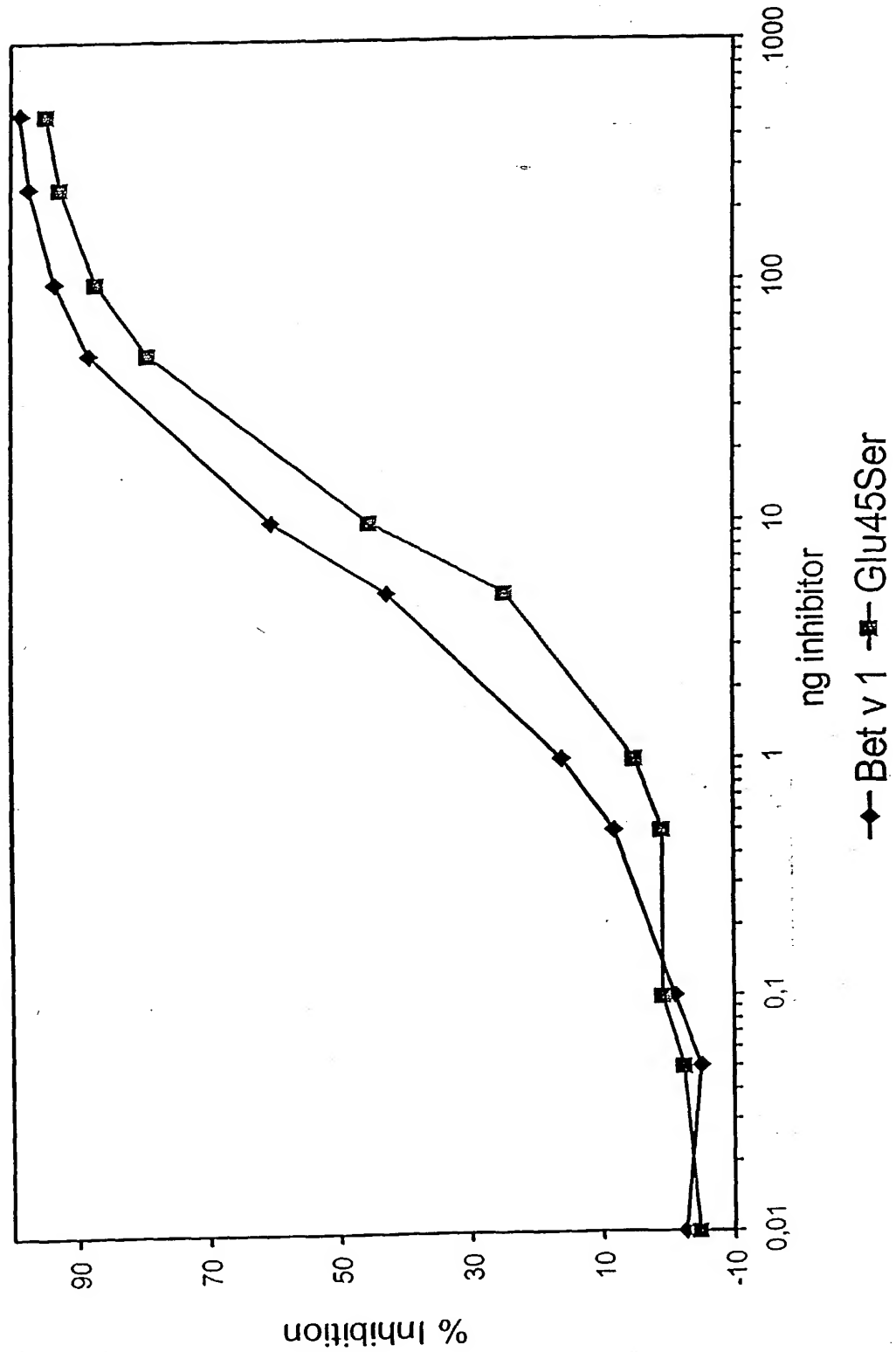
GAGATAAAGATAGTGGCAACCCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC 360
E I K I V A T P G D G G S I L K I S N K Y 120

CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGGC 420
H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAACATA 480
E T L L R A V E S Y L L A H S D A Y N stop 159



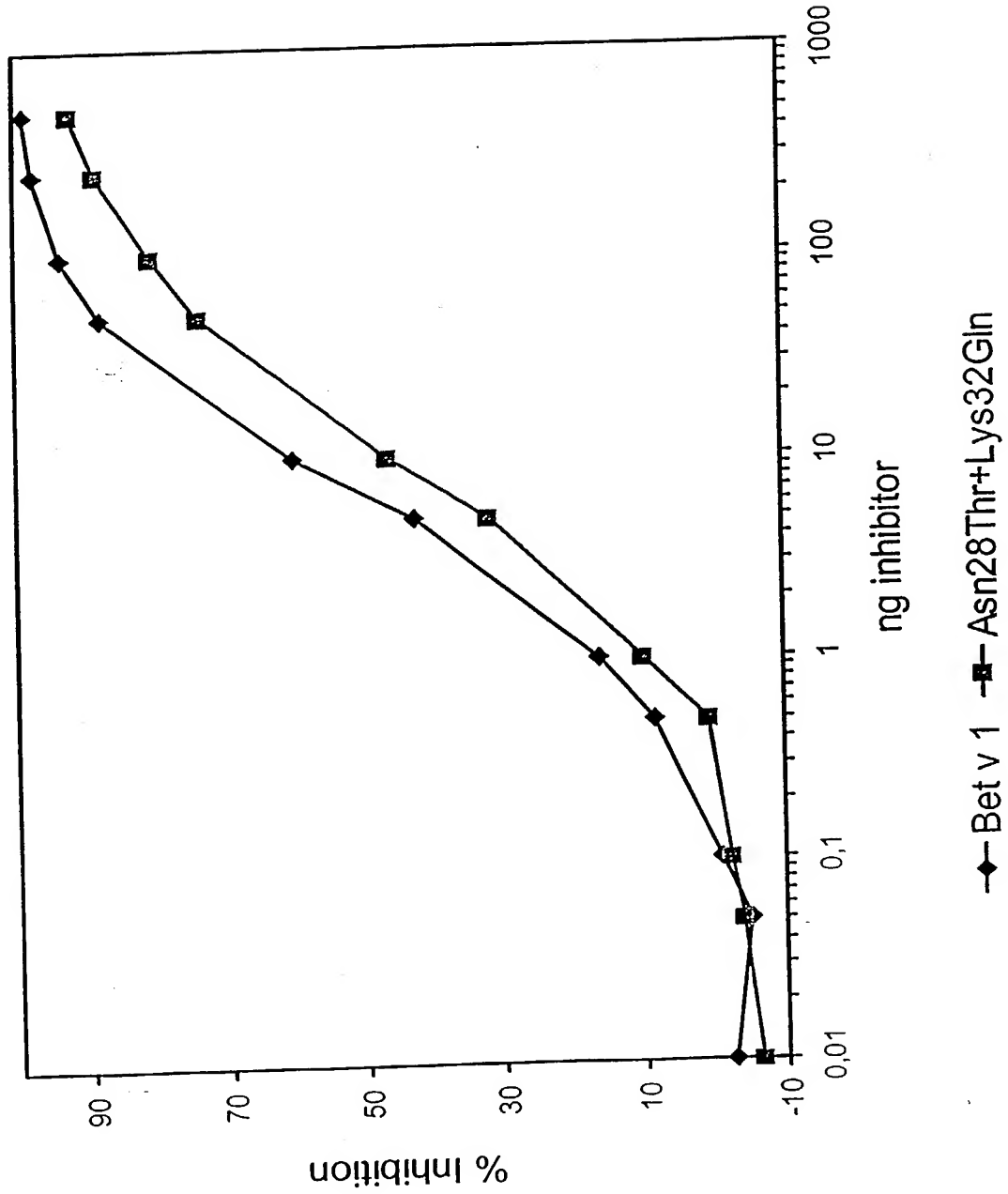
FIG. 4



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FIG. 5



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FIG. 6

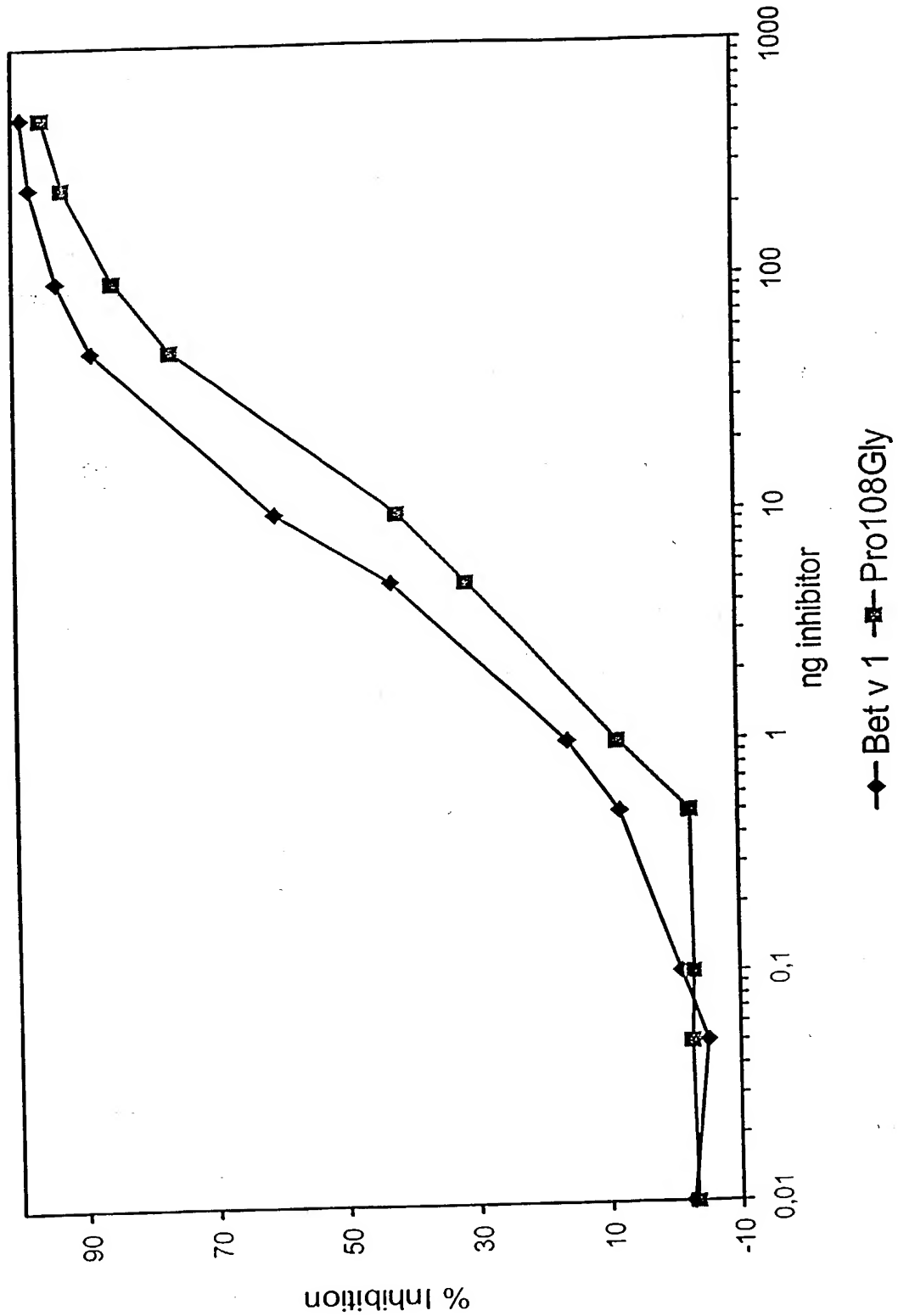
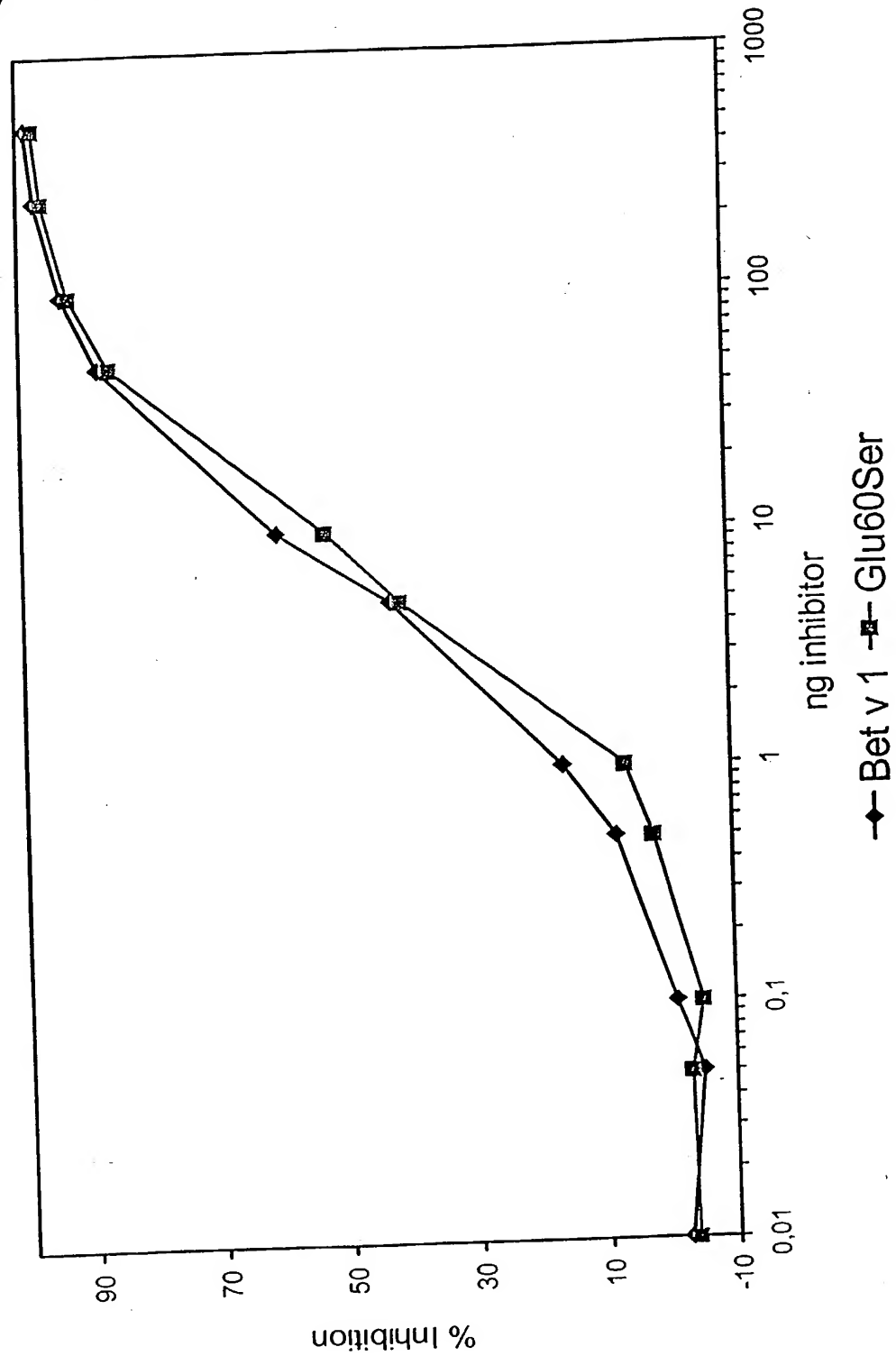




FIG. 7



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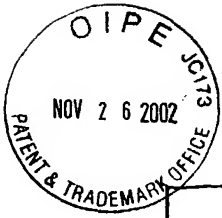
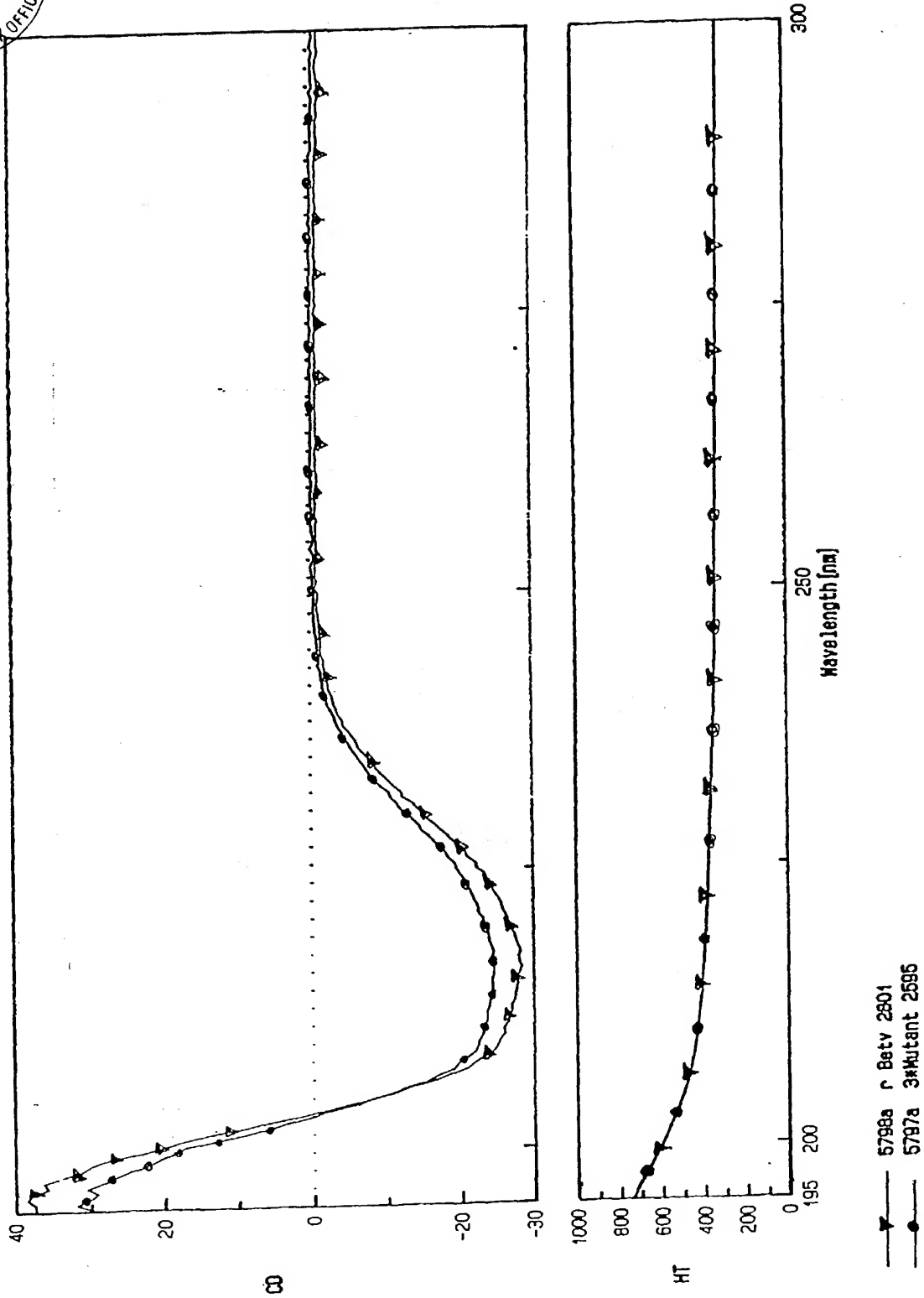
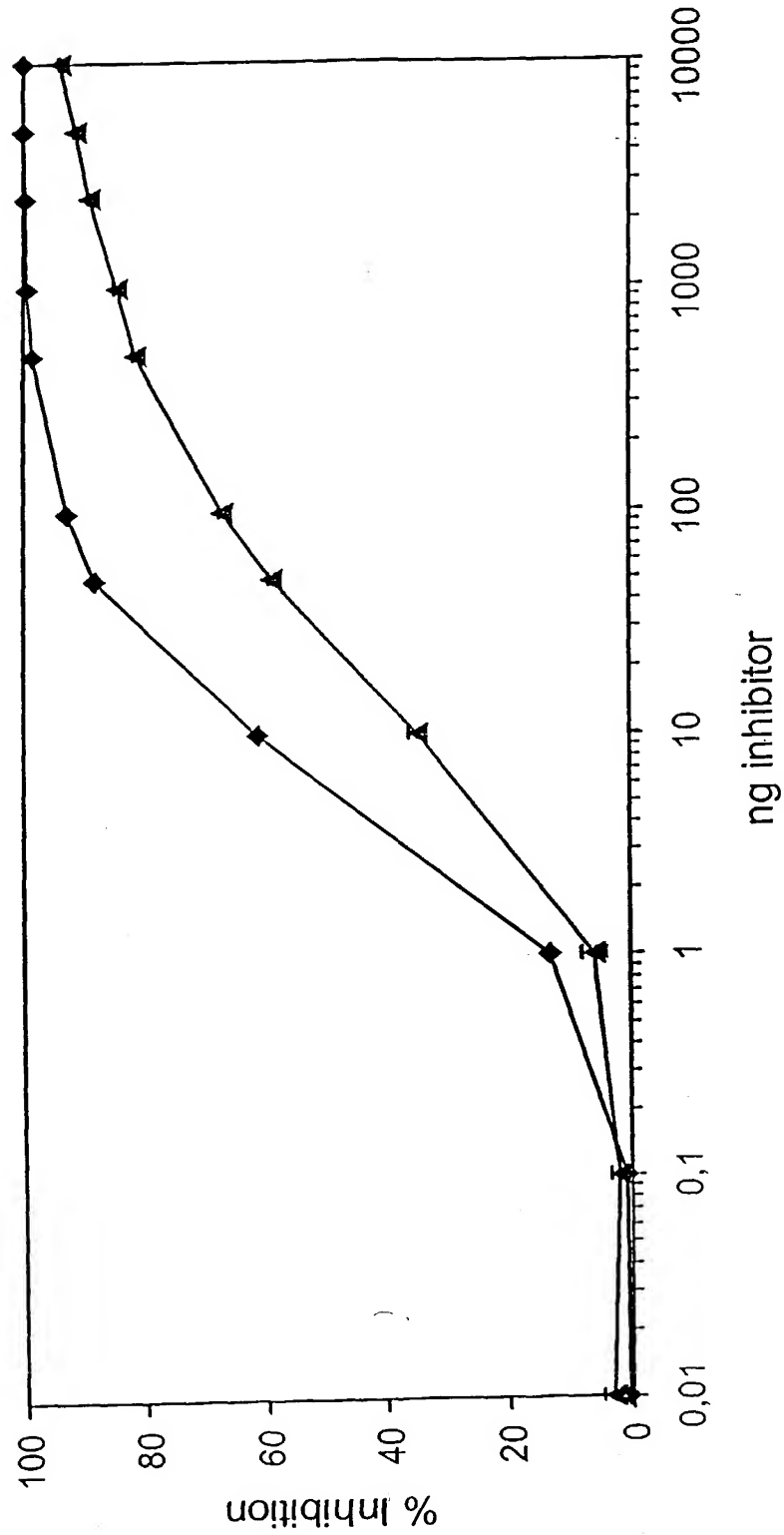


FIG. 8



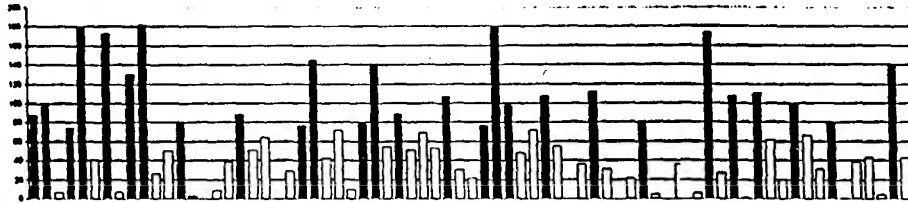
**FIG. 9**

—◆— Bet v 1 —▲— Glu45Ser, Pro108Gly, Asn28Thr+Lys32Gln.

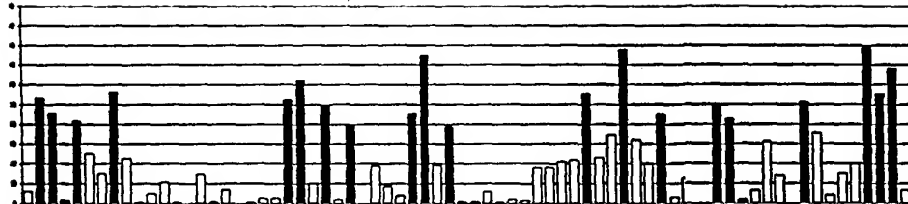
10/001,245



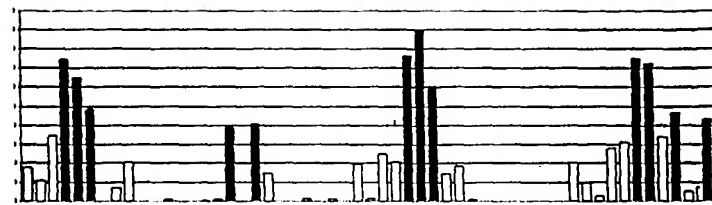
FIG. 10 A



Grid of small, illegible text, likely a data table or legend corresponding to the bar chart above.



Grid of small, illegible text, likely a data table or legend corresponding to the bar chart above.

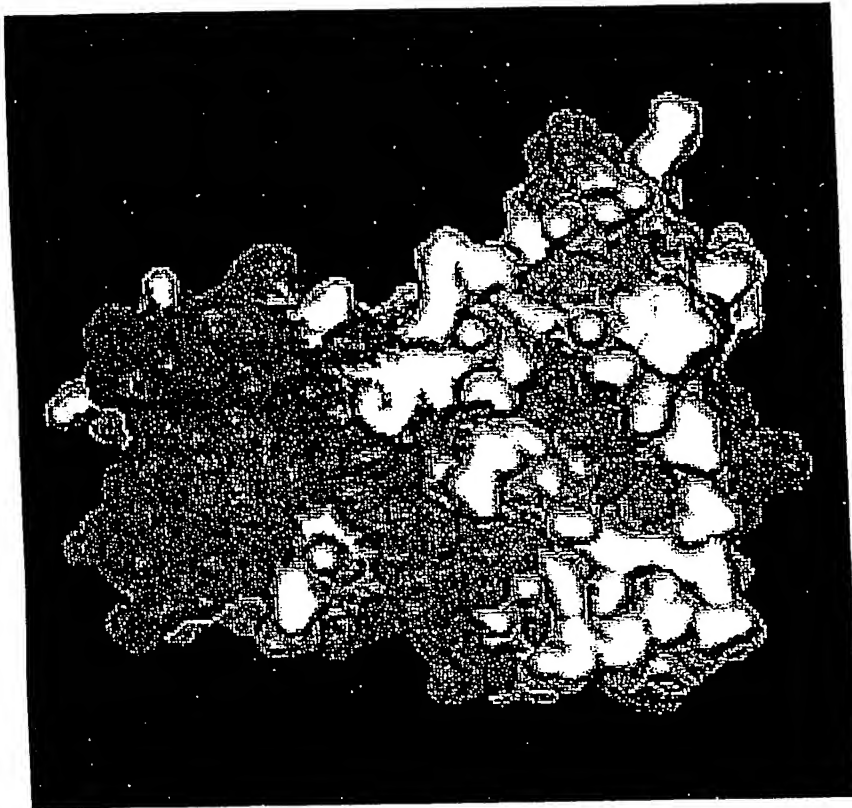


Grid of small, illegible text, likely a data table or legend corresponding to the bar chart above.

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FIG. 10 B



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FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCTGGAGGTCGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCGGCTAATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTCGCCGATTATAC	-5'

FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCAGTGCTATGAACGTCCCTAC	-5'
sense primer	5'-	TGTCAAGCTGGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCCGACCAGTG	-5'

FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAATAAAATG
 L E K R N N Y C K I K
 Kex2 cleavage site amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
all non-sense 7: CT-pPICZαA, 21-mer				5'-ATTCATCAGCTGCGAGATAGG

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FIG. 13

1	AACAATTATTGTAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G <u>G</u> V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
	1 [K72A] (AAG-GCT)	
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
	2 [Y96A] (TA-GC)	
241	GACGAGTTAGCTTATGTCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAATATCAGGTTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTTGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204



FIG. 14

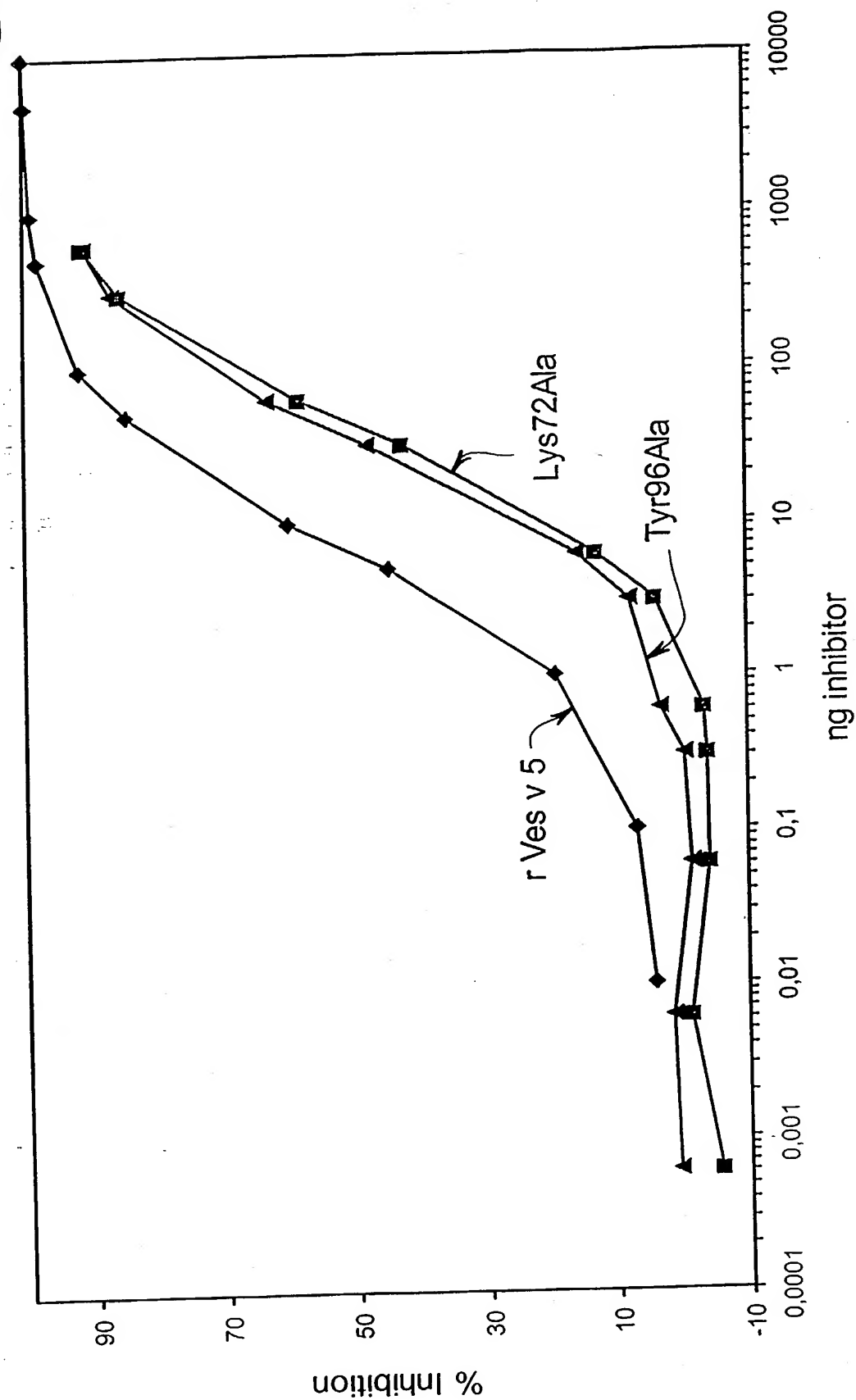
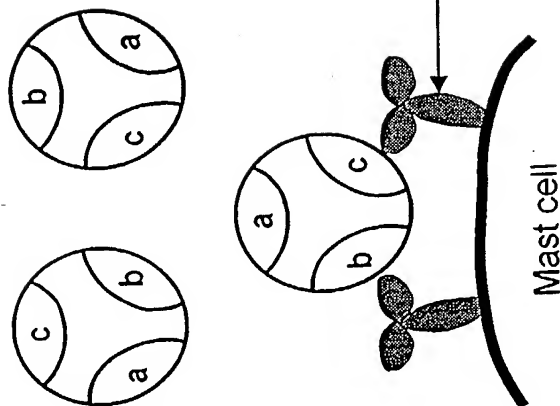
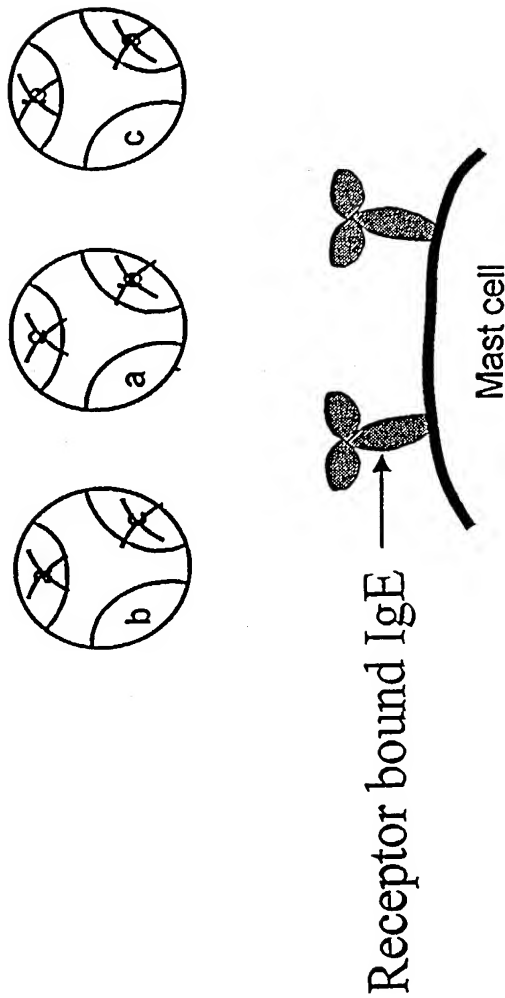


FIG. 15 A



Cross-linking

FIG. 15 B



No cross-linking





FIG. 16 A

DNA SEQUENCE

ORIGIN

```

1      cacaaattct tcttcttcc ttactactga tcattaatct gaaaacaaaa ccaaacaac
61     cattcaaaat gatgtacaaa atttgtgtc ttcatgtt ggtcgagcc gttgctgtg
121    atcaagtga tgtcaaagat tgtgccaatc atgaaatcaa aaaagtttg gtaccaggat
181    gccatggtc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccgtt
241    tcgaagccaa caaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatggt
301    tagaagtga tgttcccggt atcgatccaa atgcatgcc ttacatgaaa tgccattgg
361    ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaatt
421    ctgaaaatgt tgcgtcact gttaaagta tgggtgatga tgggttttg gcctgtgcta
481    ttgtactca tgctaaaatc cgcgattaaa tcaaacaaaa ttattgatt ttgtaatcac
541    aatgattga ttttcttcc aaaaaaaaaa taaataaaat ttgggaatt c

```

FIG. 16 B

```

1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrkg pfqleavfea
61     nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen
121    vvvtkvmgd dgvlaciat hakird

```


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FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.

331pMalc (s)
 189BV (a)
 188BV (s)
 362BV (a)
 361BV (s)
 364BV (a)
 363BV (s)
 366BV (a)
 365BV (s)
 332pMalc (a)

FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

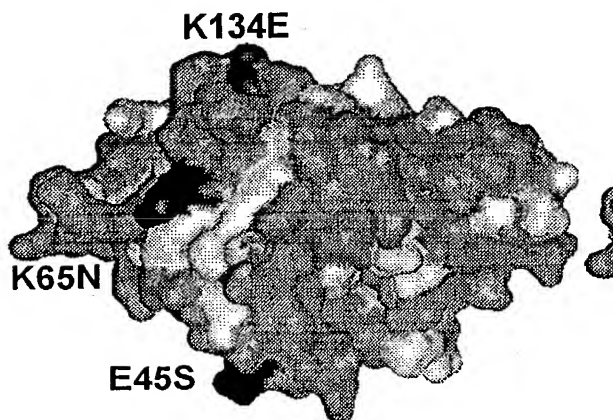
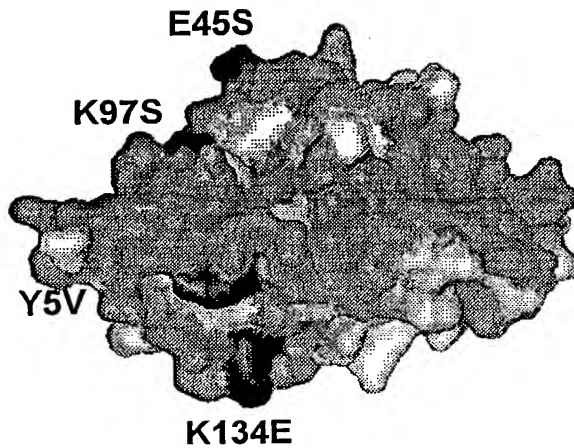
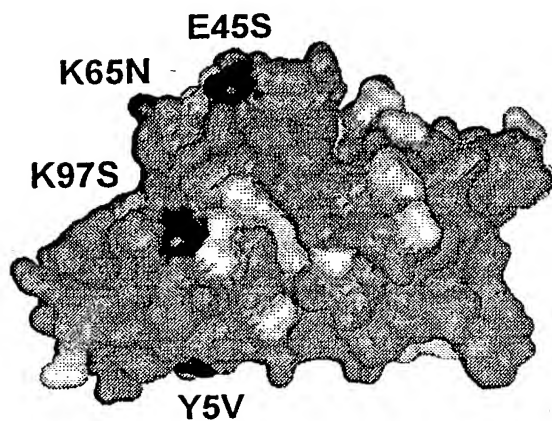
331pMalc
 368BVa
 367BVa
 370BVa
 369BVa
 372BVa

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FIG. 19 A

Bet v 1 (2628)

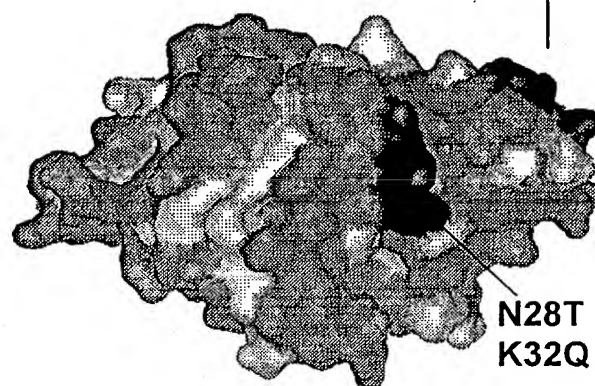
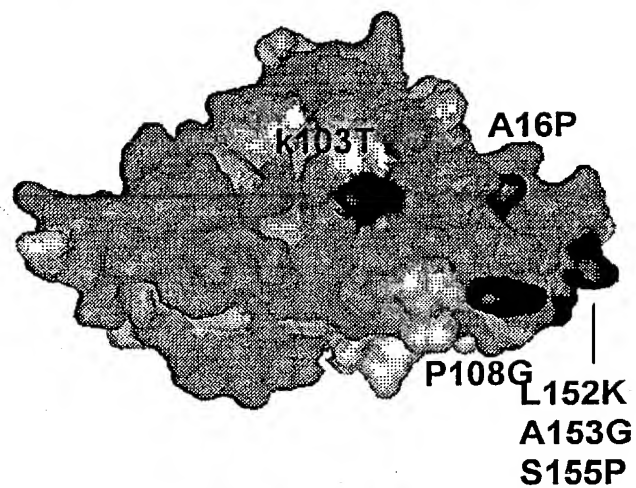
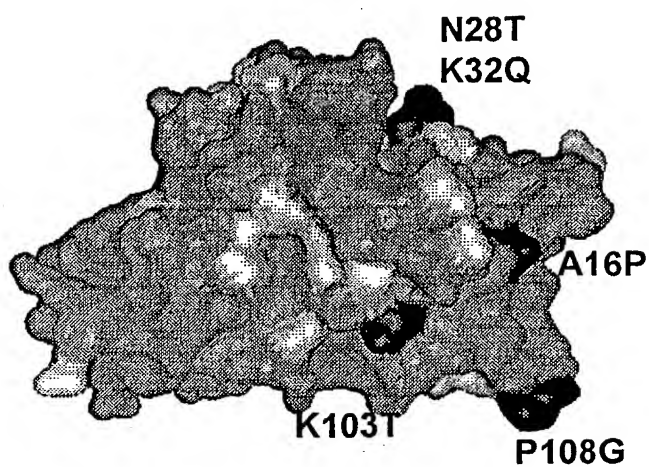


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FIG. 19 B

Bet v 1 (2637)



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FIG. 20

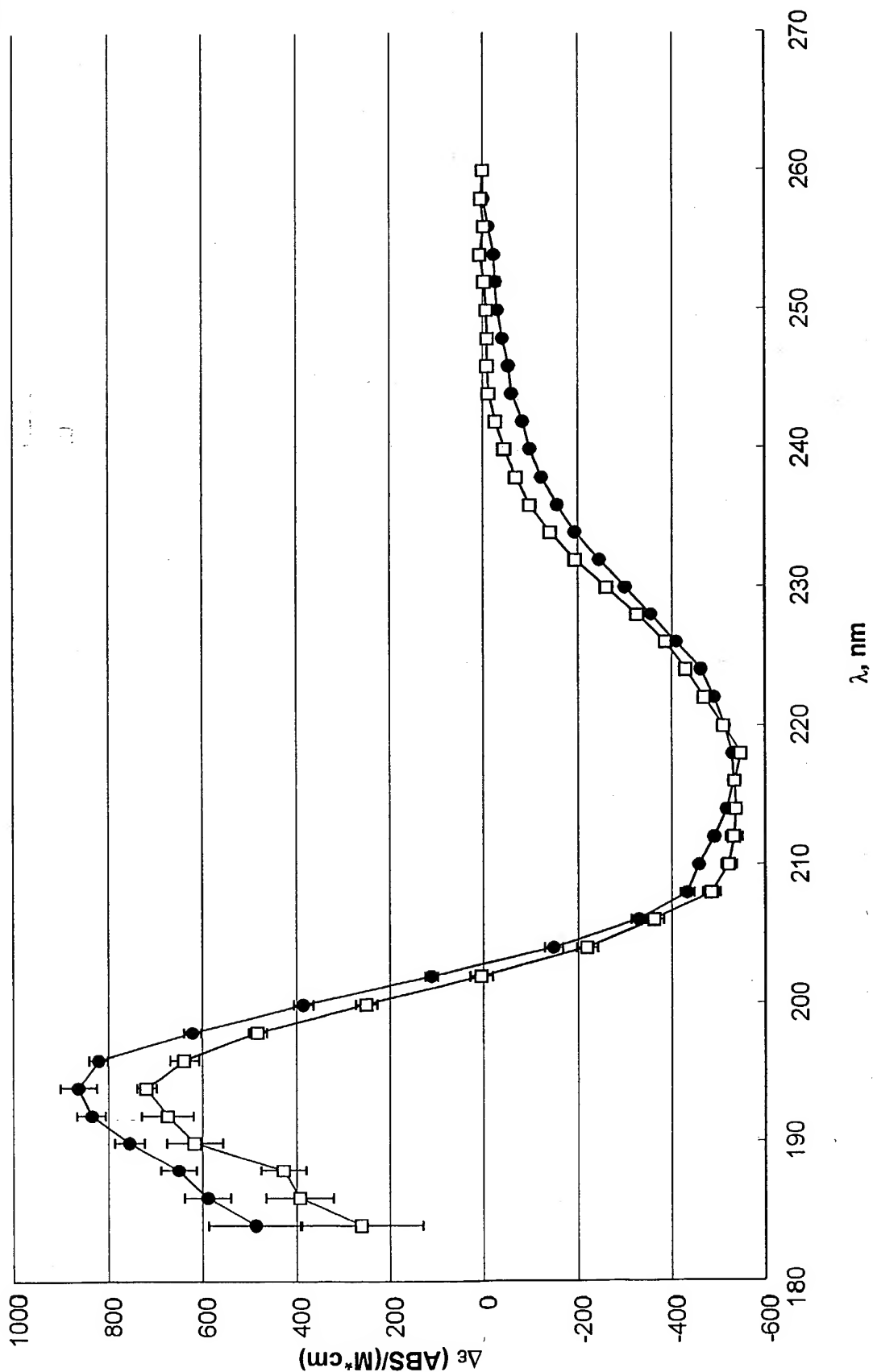
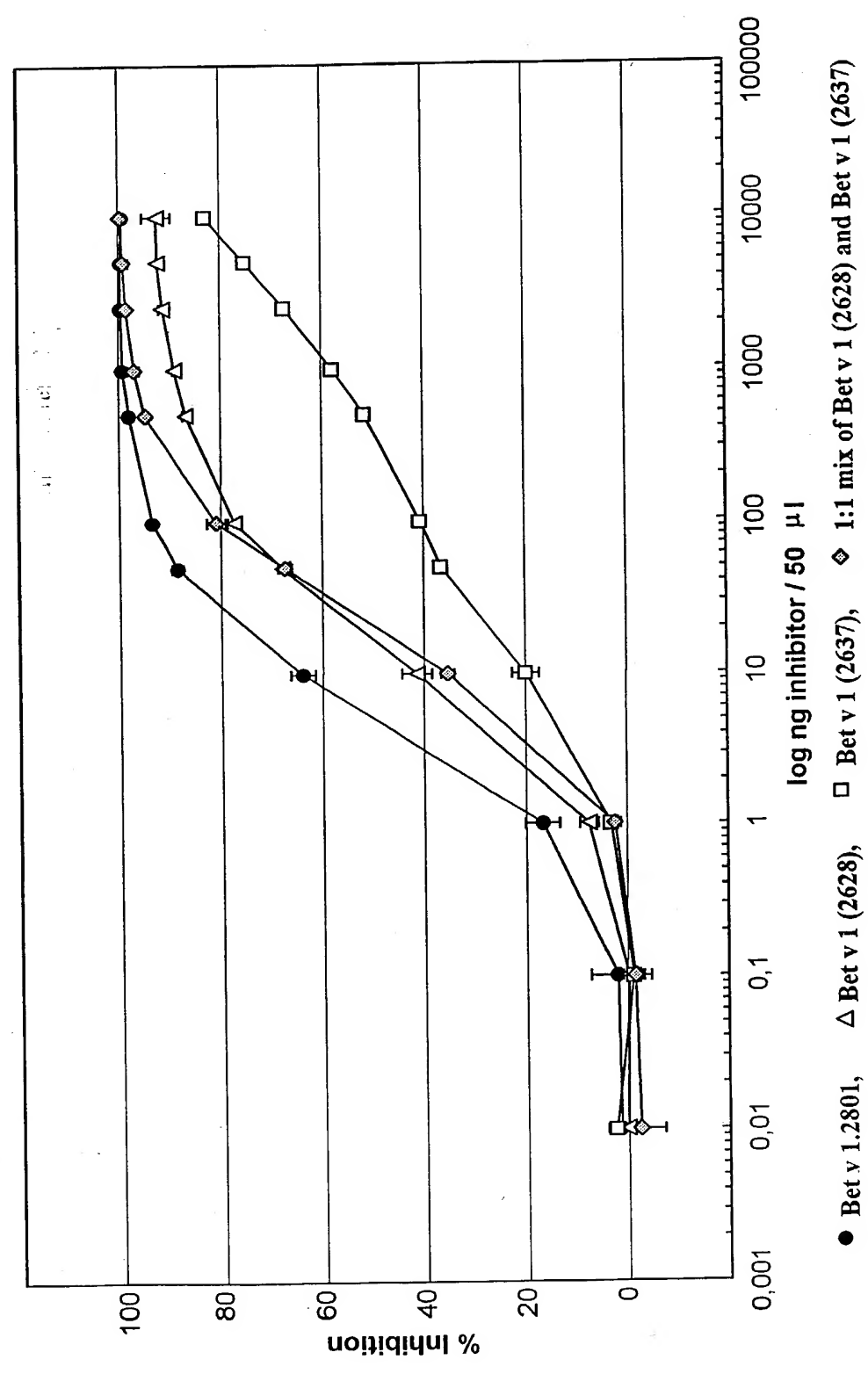




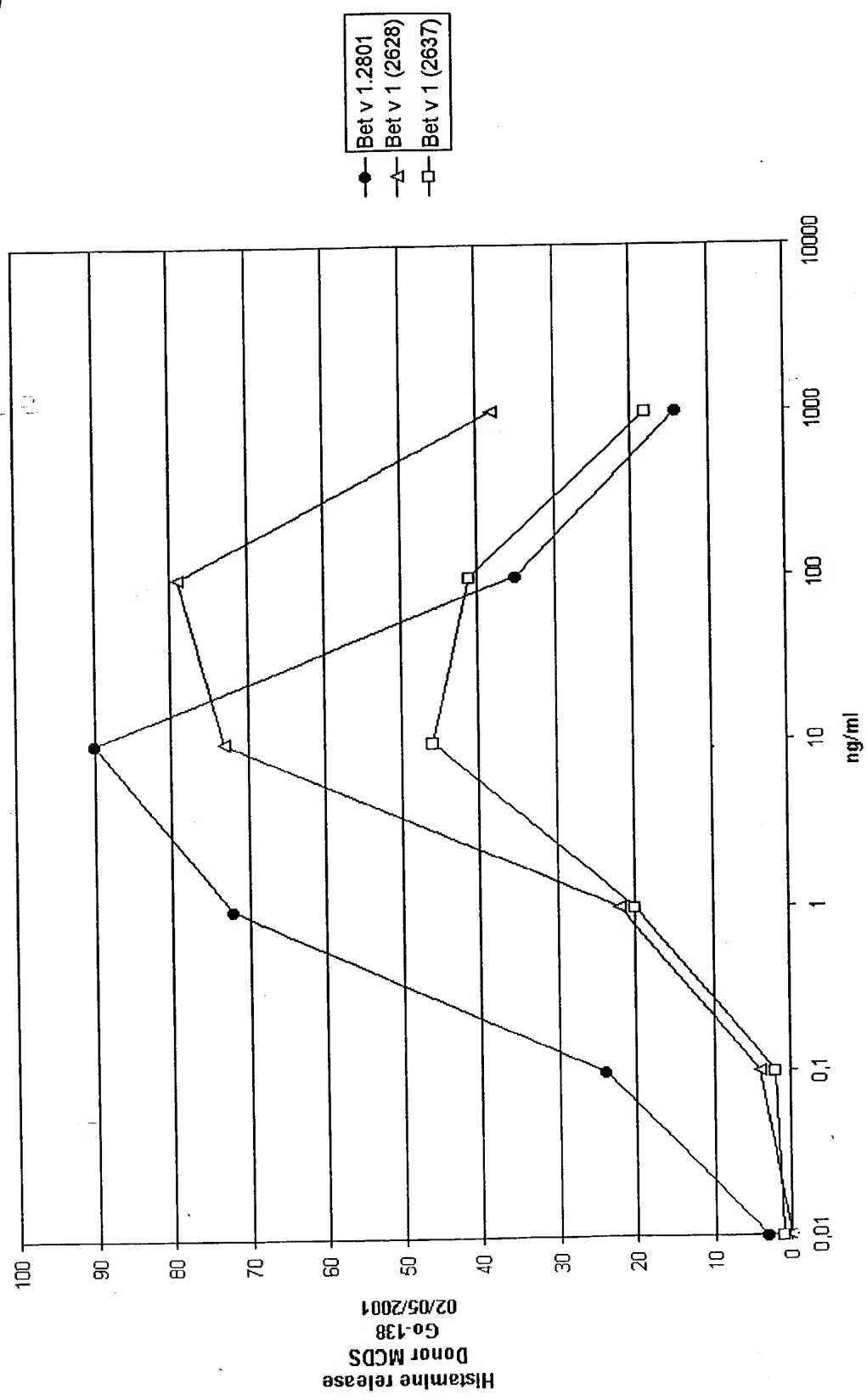
FIG. 21



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FIG. 22



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FIG. 23

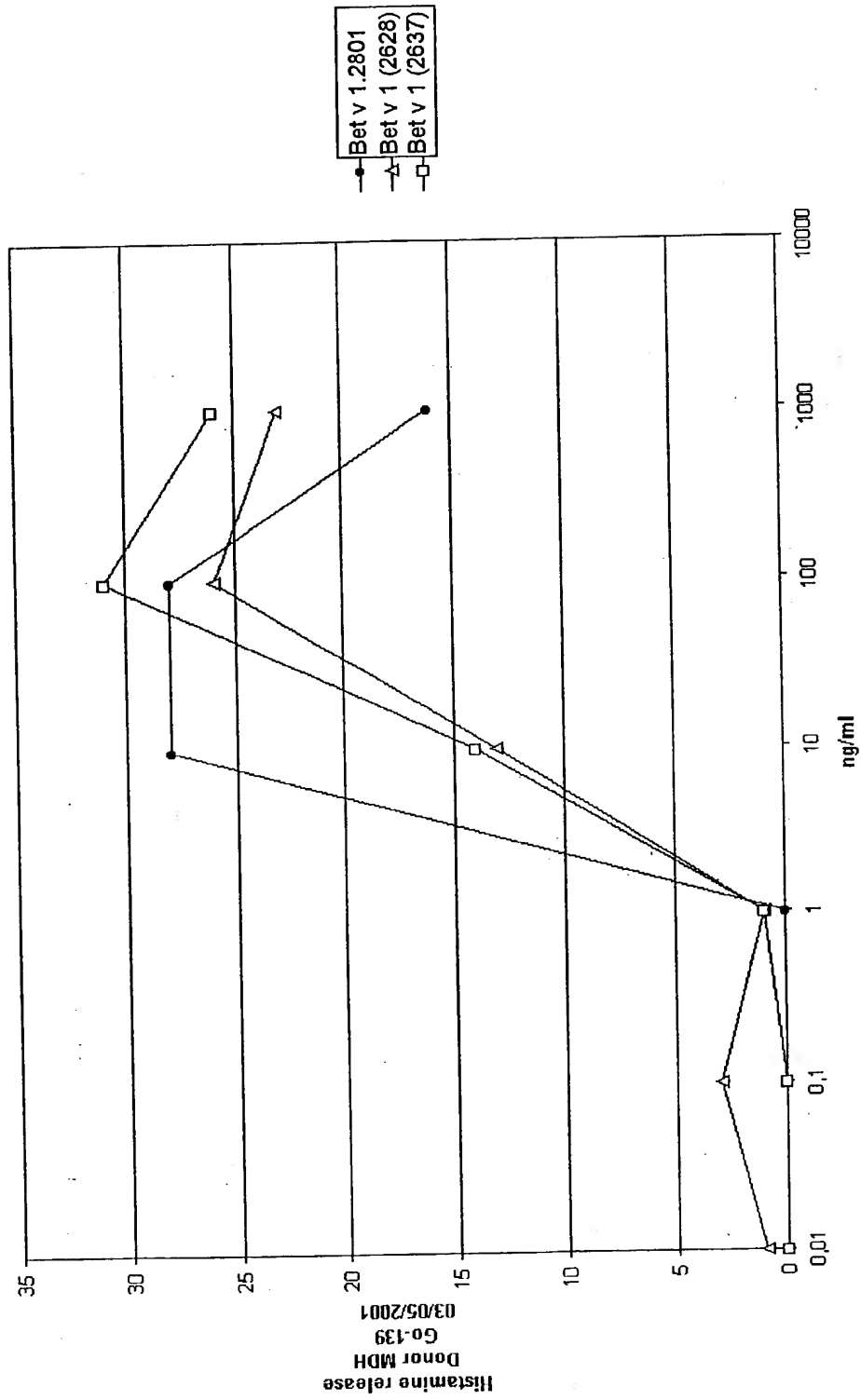




FIG. 24

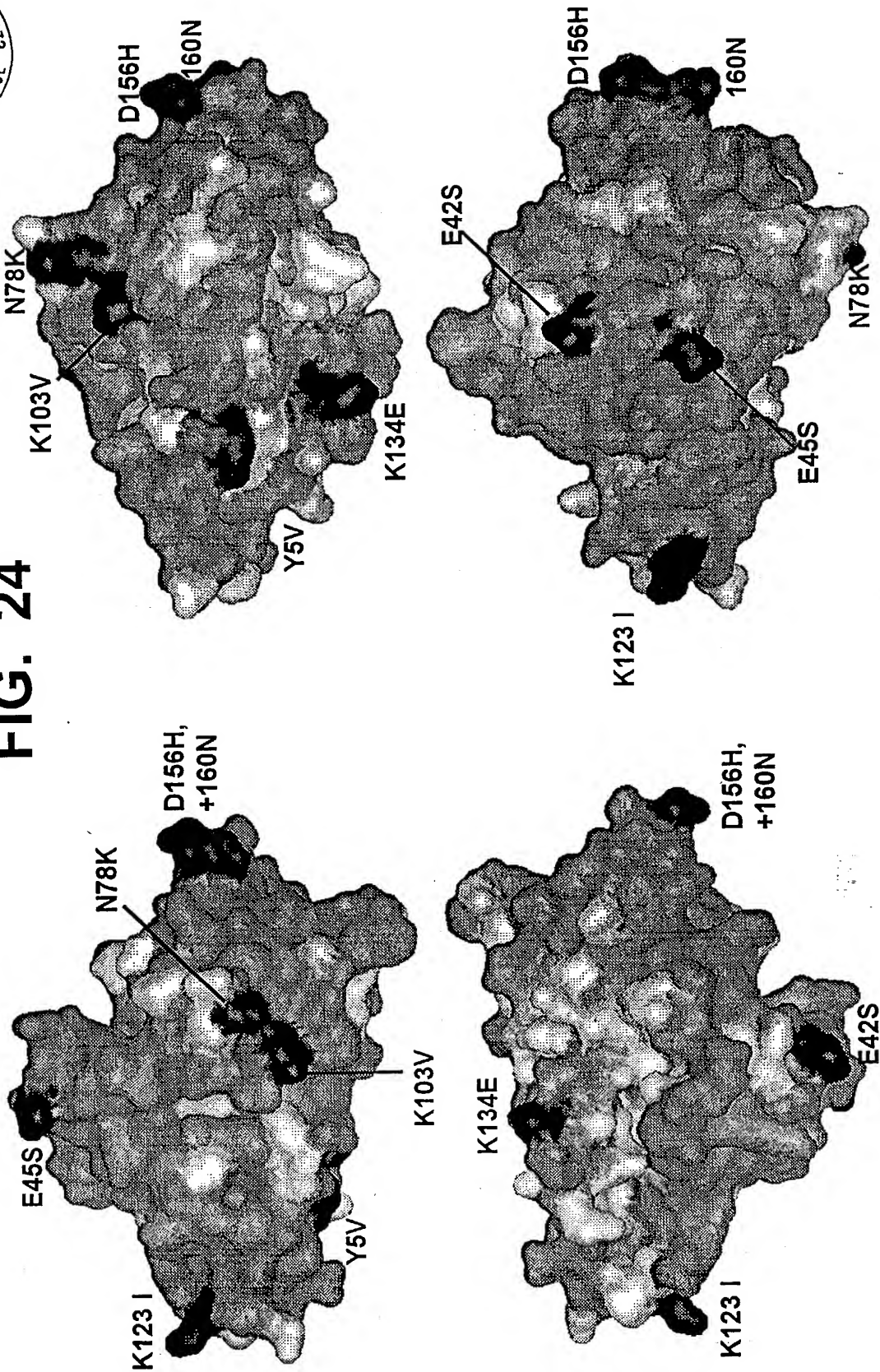
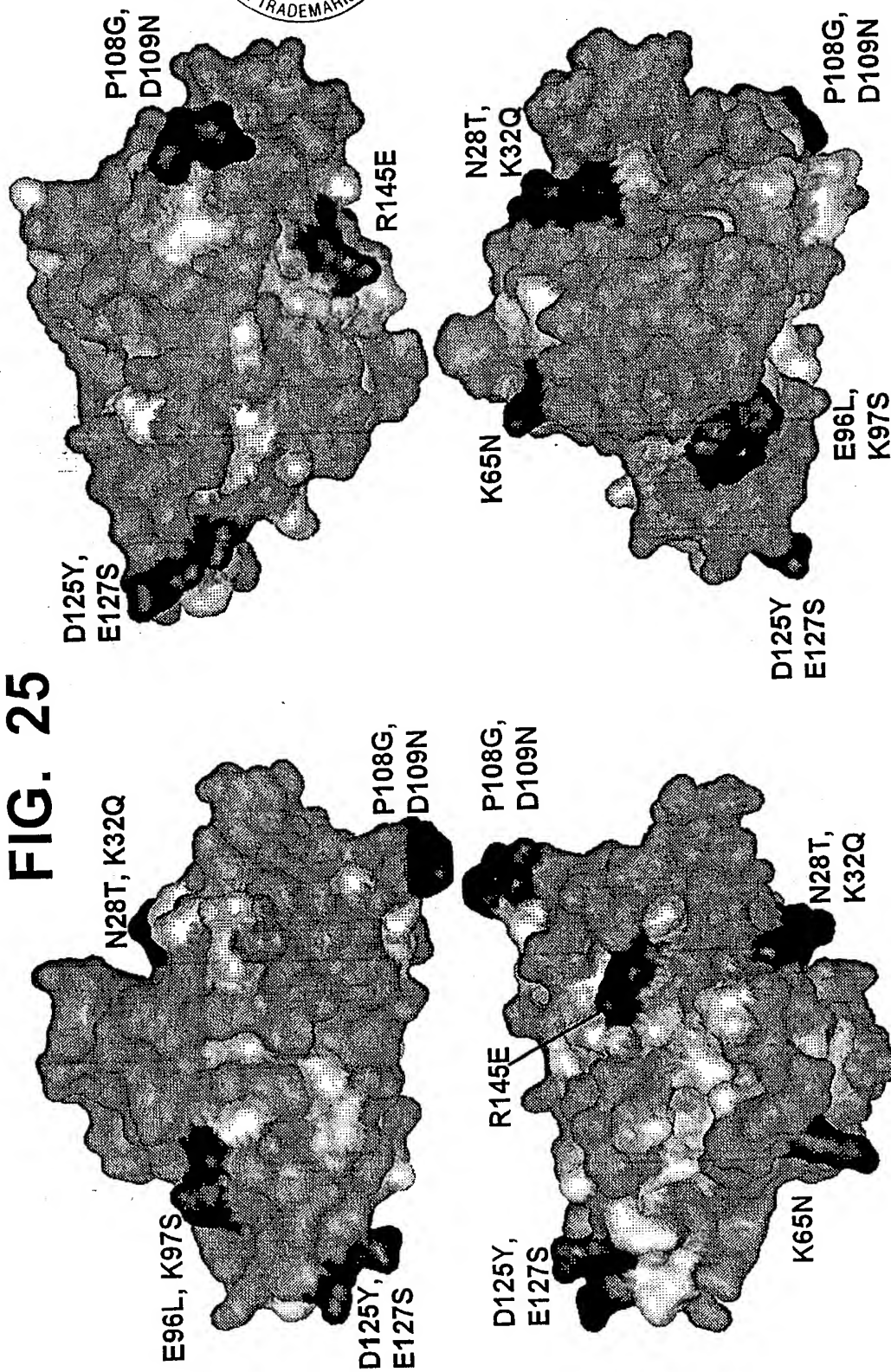


FIG. 25



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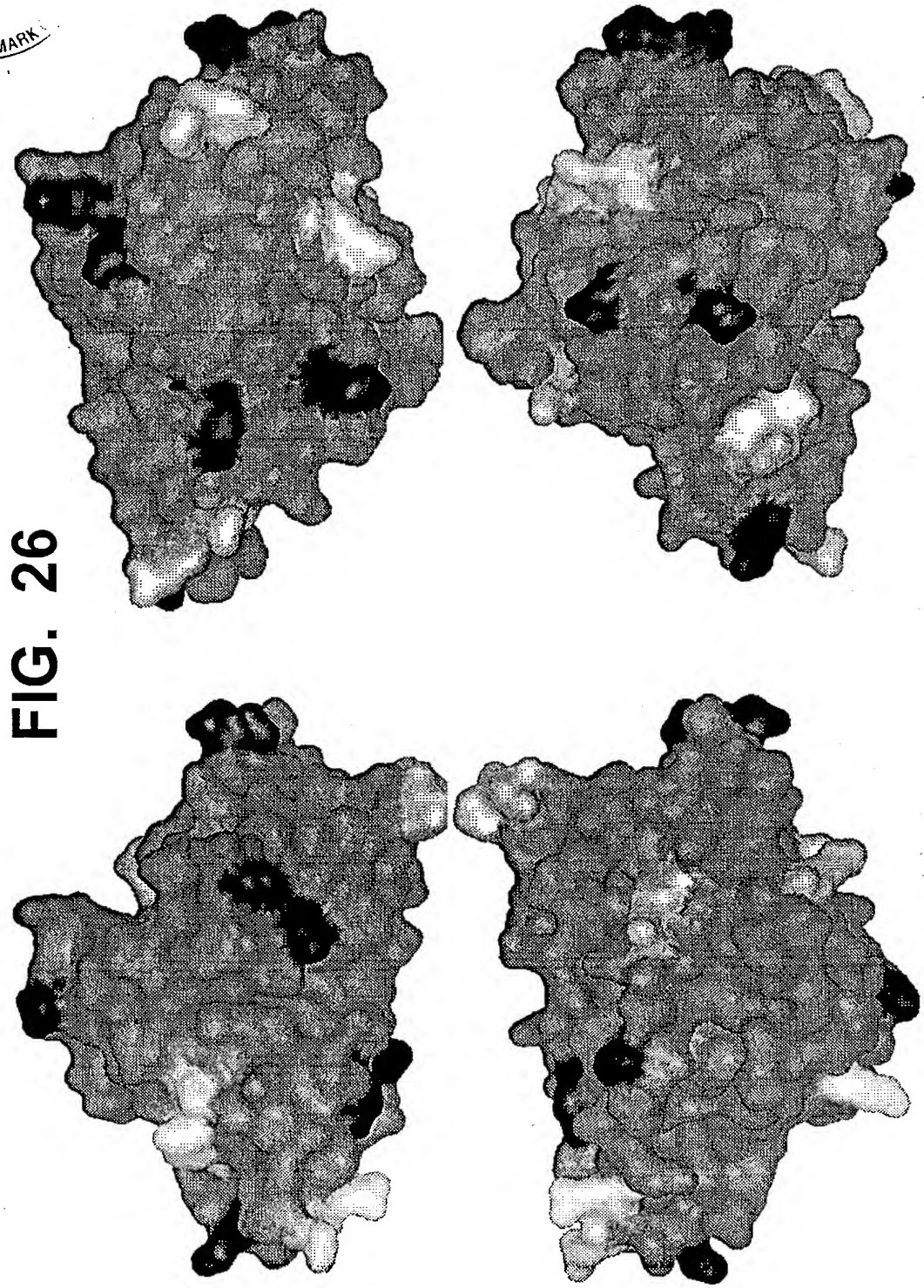
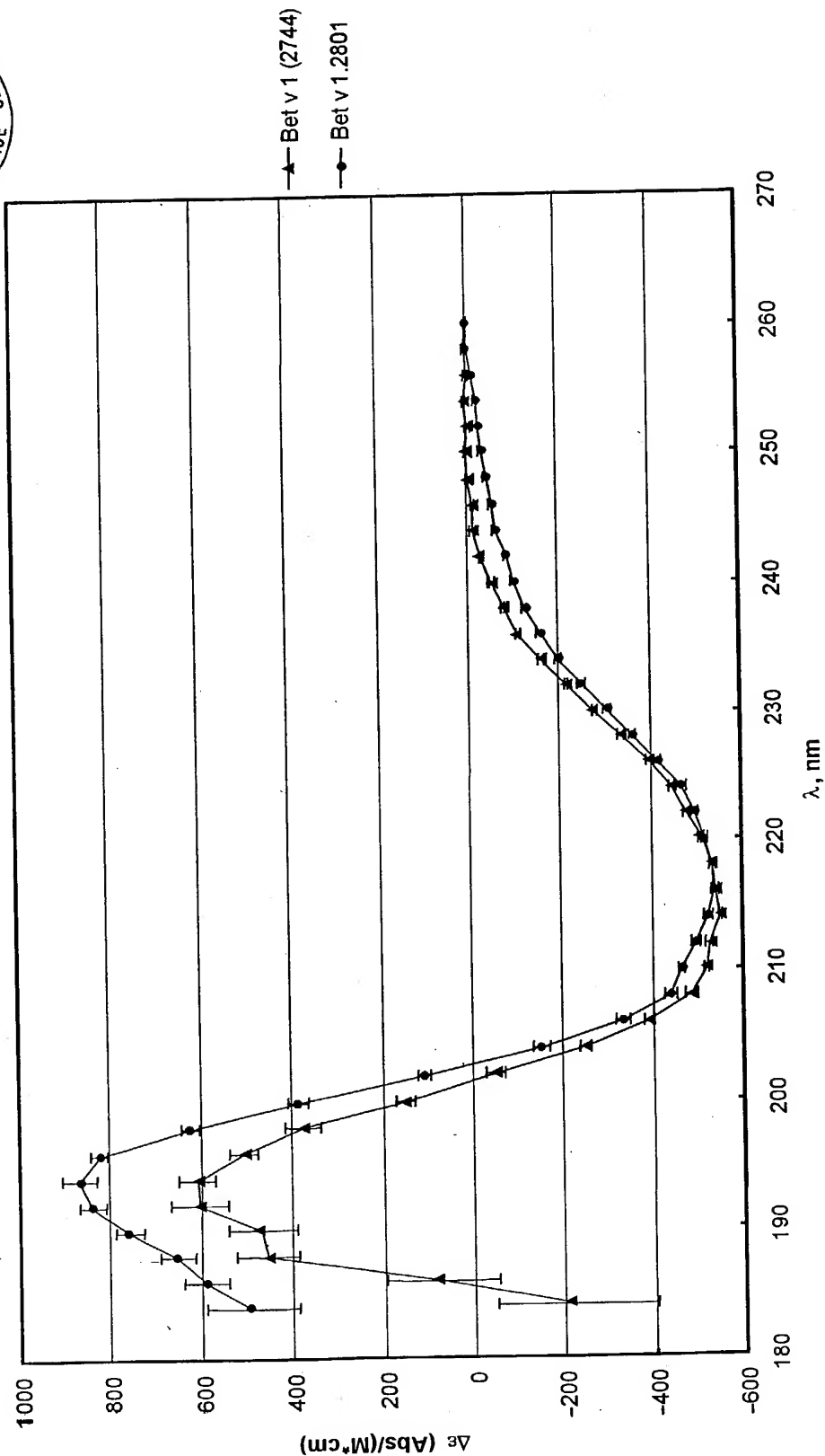


FIG. 26

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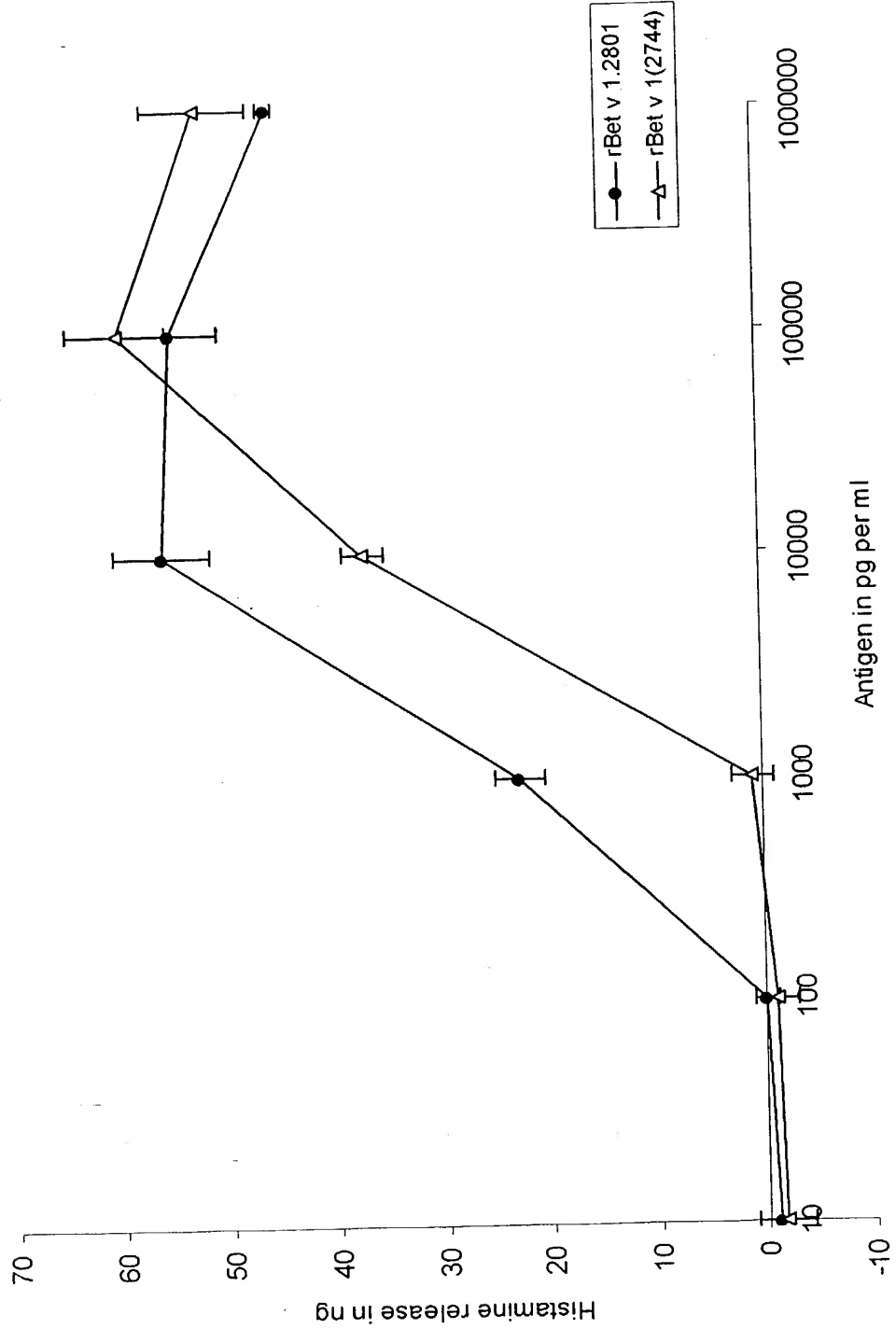
FIG. 27



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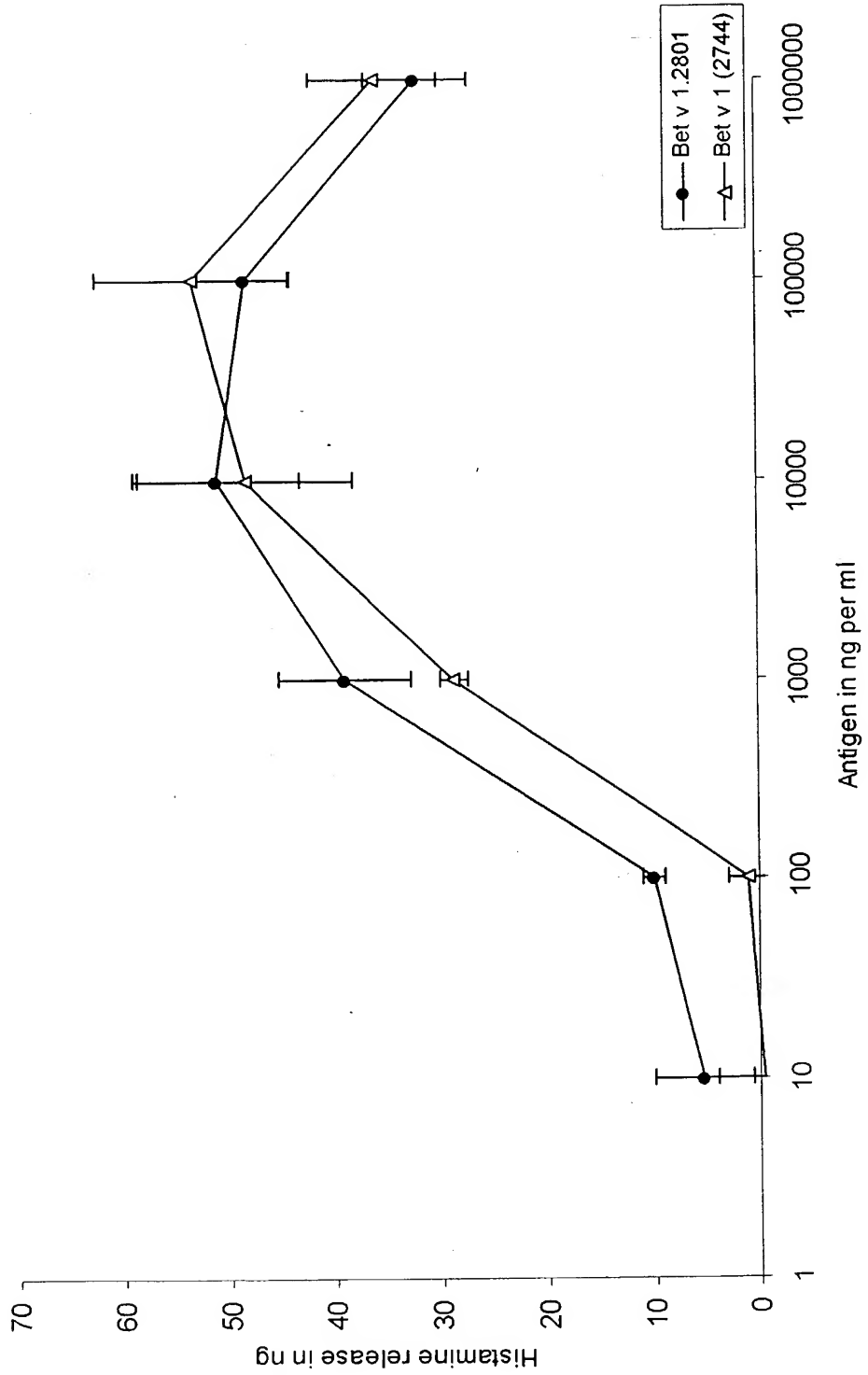
FIG. 28



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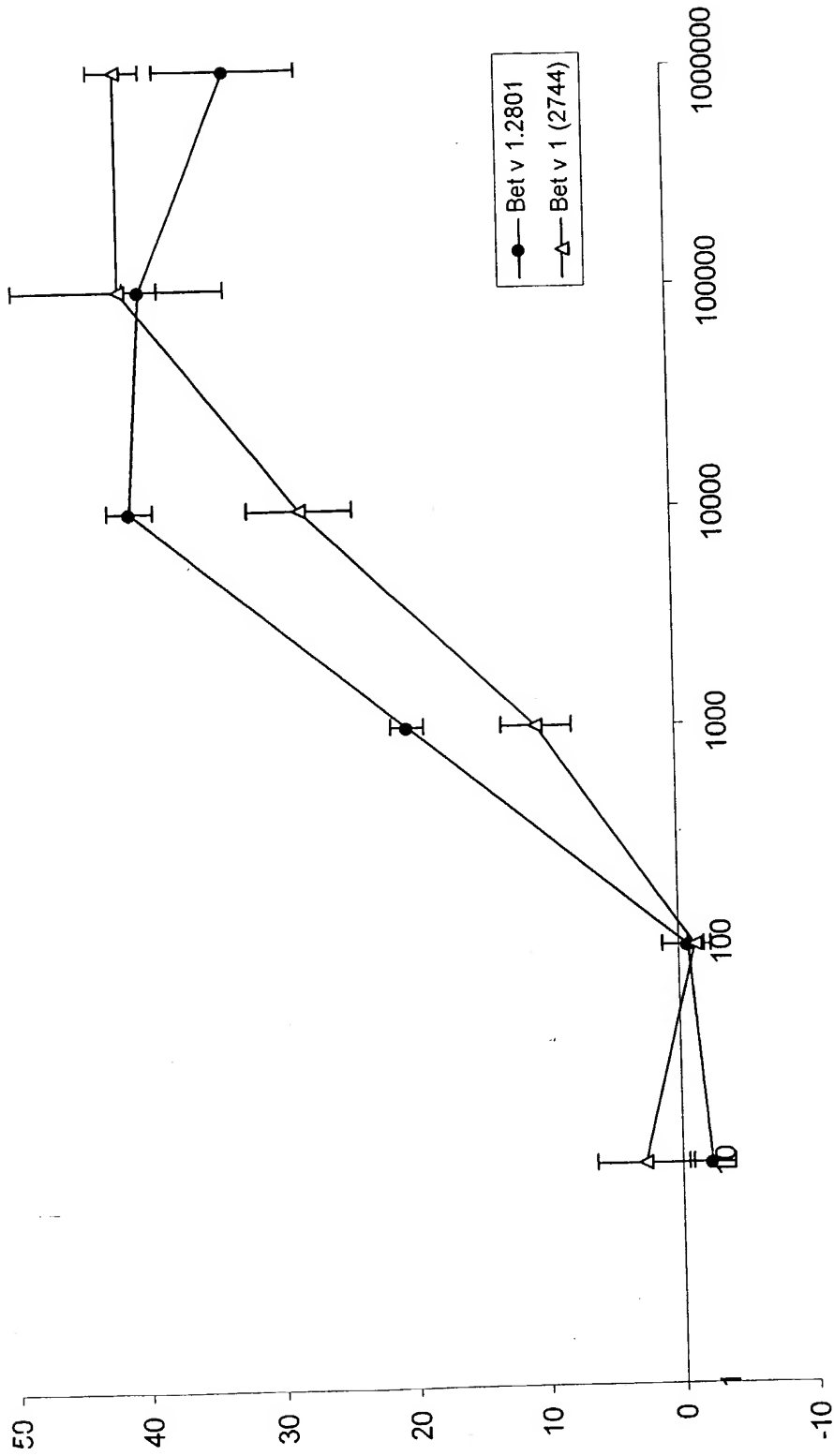
FIG. 29 A



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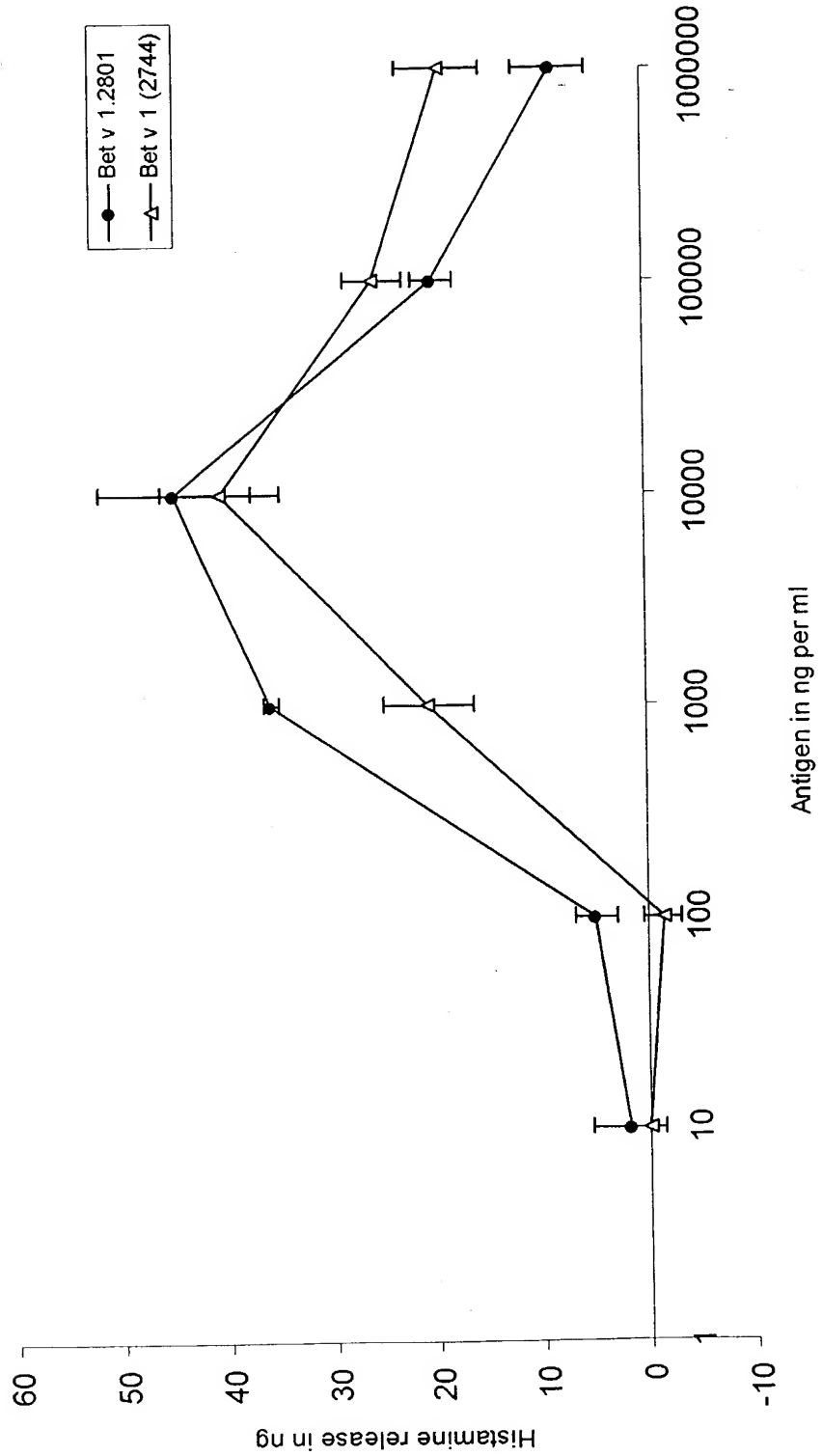
FIG. 29 B



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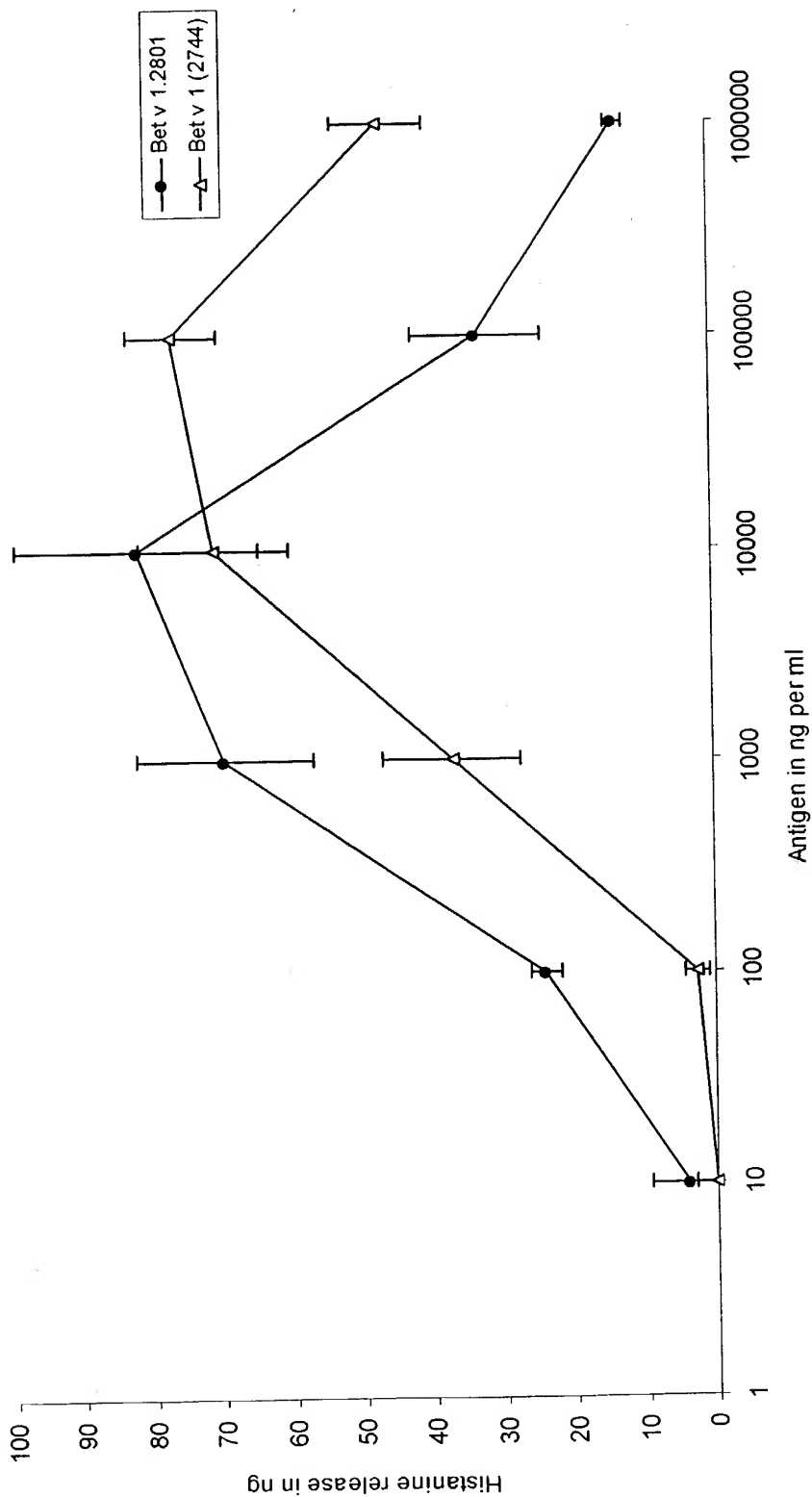
FIG. 29 C



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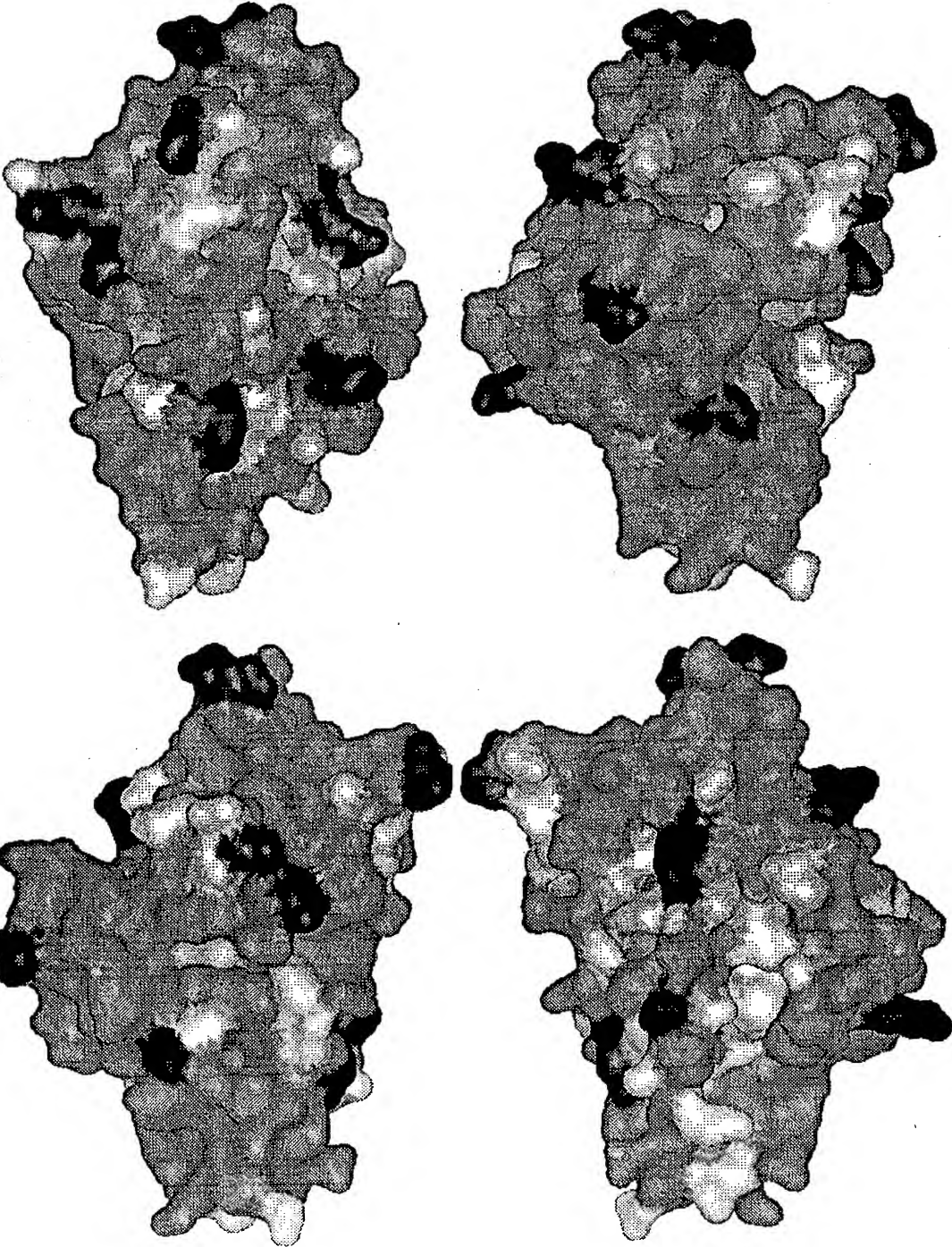
FIG. 29 D



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FIG. 30



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FIG. 31

K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	5' -CGGGGTACCAGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	5' -CATGGCATGCAATTACATGAAATGCCCATTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	5' -CTACGCATGCCATTACATGAAATGCCCATTTGGTTAATGGACAA CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'



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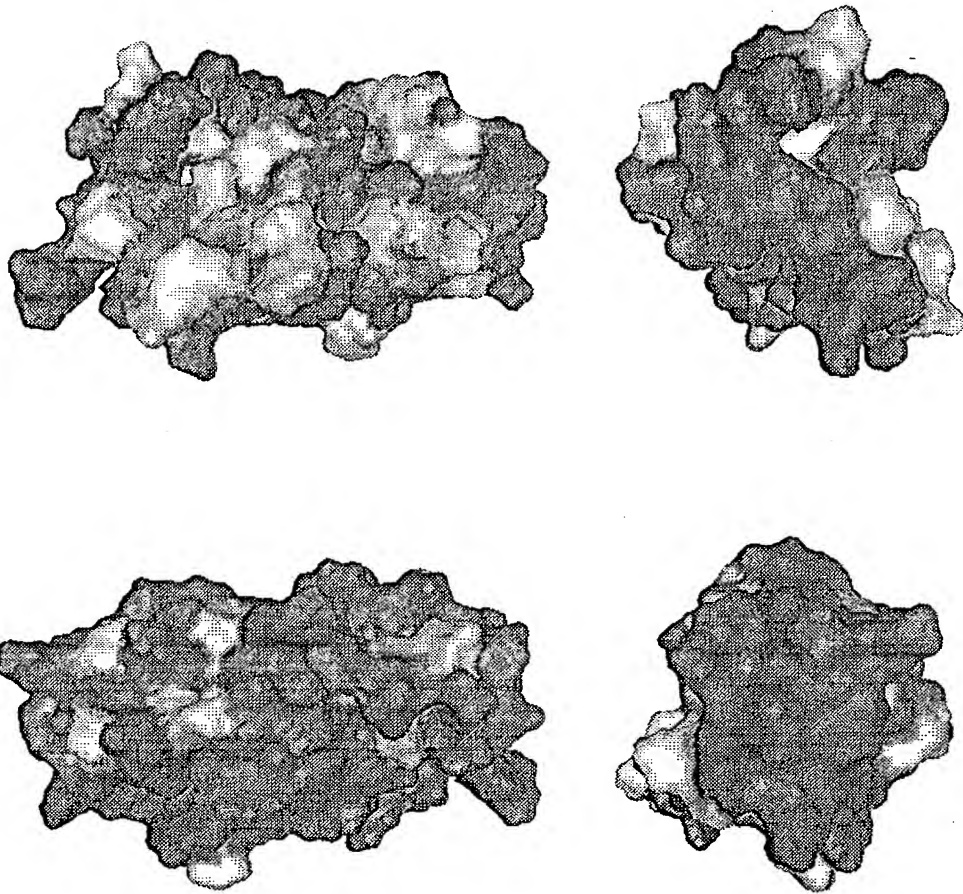
FIG. 32

	1	10	1	10	2	3
1 DERP2-ALK-G Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
2 DERP2-CONA Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
3 DERP2-ISO101 Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
4 DERP2-ISO102 Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
5 DERP2-ISO104 Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
6 DERP2-ISO113 Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
7 DERP2-ISO120 Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
8 1A9V Der p 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
9 DER2-DEFA Der f 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
10 B61241 Der f 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
11 1AHK Der f 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
12 A61501 Der f 2	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
13 O96430 Eur m 20101 O96430	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
14 O97ZZ Eur m 20102 O97ZZ	DQV	VK	DC	AN	HE	IKKVLVPGCHGSEPCIIH
	40	50	60	70	80	
1 DERP2-ALK-G Der p 2	RGK	PF	Q	L	E	A
2 DERP2-CONA Der p 2	RGK	PF	Q	L	E	A
3 DERP2-ISO101 Der p 2	RGK	PF	Q	L	E	A
4 DERP2-ISO102 Der p 2	RGK	PF	Q	L	E	A
5 DERP2-ISO104 Der p 2	RGK	PF	Q	L	E	A
6 DERP2-ISO113 Der p 2	RGK	PF	Q	L	E	A
7 DERP2-ISO120 Der p 2	RGK	PF	Q	L	E	A
8 1A9V Der p 2	RGK	PF	Q	L	E	A
9 DER2-DEFA Der f 2	RGK	PF	Q	L	E	A
10 B61241 Der f 2	RGK	PF	Q	L	E	A
11 1AHK Der f 2	RGK	PF	Q	L	E	A
12 A61501 Der f 2	RGK	PF	Q	L	E	A
13 O96430 Eur m 20101 O96430	RGK	PF	Q	L	E	A
14 O97ZZ Eur m 20102 O97ZZ	RGK	PF	Q	L	E	A
	90	100	110	120		
1 DERP2-ALK-G Der p 2	VKG	Q	Y	D	I	K
2 DERP2-CONA Der p 2	VKG	Q	Y	D	I	K
3 DERP2-ISO101 Der p 2	VKG	Q	Y	D	I	K
4 DERP2-ISO102 Der p 2	VKG	Q	Y	D	I	K
5 DERP2-ISO104 Der p 2	VKG	Q	Y	D	I	K
6 DERP2-ISO113 Der p 2	VKG	Q	Y	D	I	K
7 DERP2-ISO120 Der p 2	VKG	Q	Y	D	I	K
8 1A9V Der p 2	VKG	Q	Y	D	I	K
9 DER2-DEFA Der f 2	VKG	Q	Y	D	I	K
10 B61241 Der f 2	VKG	Q	Y	D	I	K
11 1AHK Der f 2	VKG	Q	Y	D	I	K
12 A61501 Der f 2	VKG	Q	Y	D	I	K
13 O96430 Eur m 20101 O96430	VKG	Q	Y	D	I	K
14 O97ZZ Eur m 20102 O97ZZ	VKG	Q	Y	D	I	K

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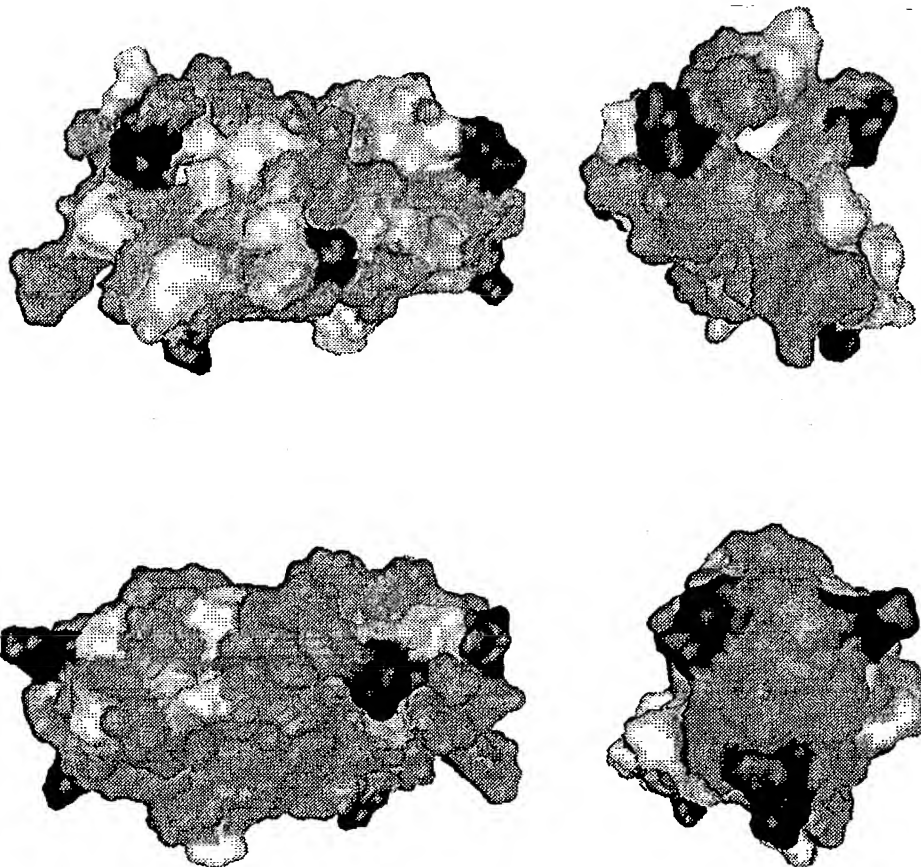
FIG. 33



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FIG. 34



	1 0 0	9 0	8 0	7 0	6 0	5 0
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						
	4 0	3 0	2 0	1 0	1 0	
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						
	2 0	3 0	4 0	5 0	6 0	7 0
Derp1 ALK						
Derp1						
Eurm 10101						
Eurm 10101						
Eurm 10102						
Derf1						
Eurm 1						
Derf1						

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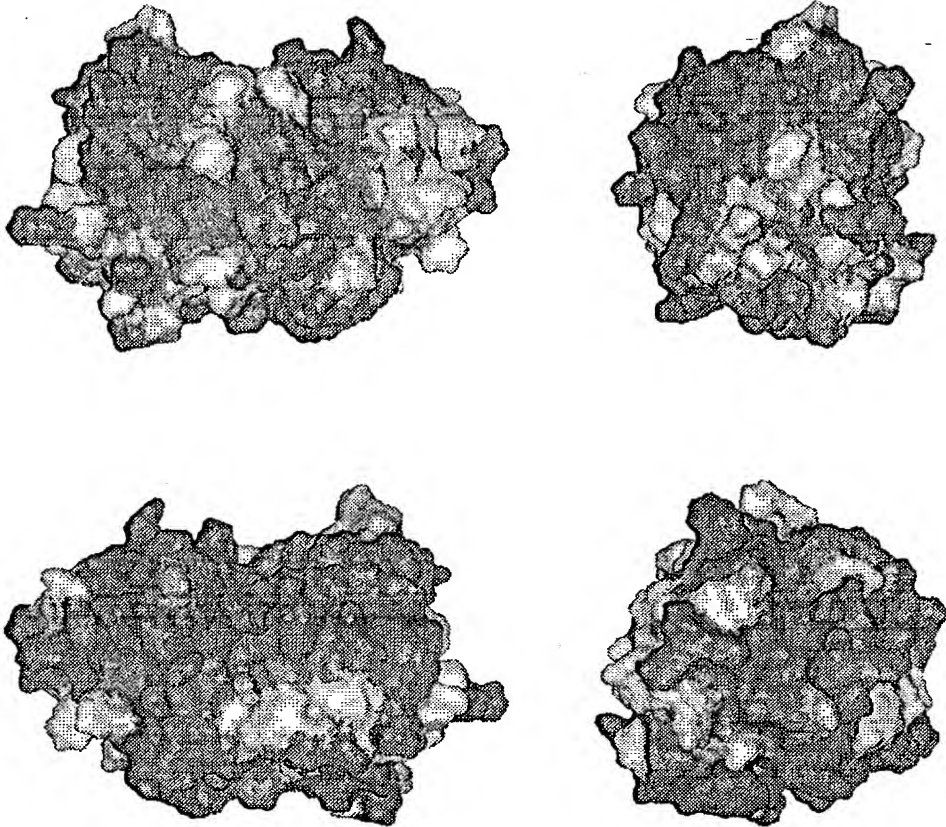
FIG. 35 B

	80	90	100	110	120	130	
Derpl ALK	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Derpl	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Eurm 1.0101	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Eurm 1.0102	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Derf1	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Eurm 1	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
Derf1	I P R G I E Y I Q H N G V V Q E S Y R Y V A R E Q S C R R P N A Q R F G I S N Y C Q I Y P P N V N K I R E A L A Q T H						
	140	150	160	170	180	190	
Derpl ALK	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T T						
Derpl	S A I A V I I G I K D L D A F R H Y D G R T I I Q R D N G Y Q P N Y H A V N I V G Y S N A Q G V D Y W I V R N S W D T T						
Eurm 1.0101	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T						
Eurm 1.0102	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T						
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T						
Eurm 1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T						
Derf1	T A V A V I I G I K D L N A F R H Y D G R T I I Q H D N G Y Q P N Y H A V N I V G Y G N T Q G V D Y W I V R N S W D T T						
	200	210	220				
Derpl ALK	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Derpl	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Eurm 1.0101	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Eurm 1.0102	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Derf1	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Eurm 1	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						
Derf1	W G D N G Y G Y F A A N I D L M M I E E Y P Y V V I L						

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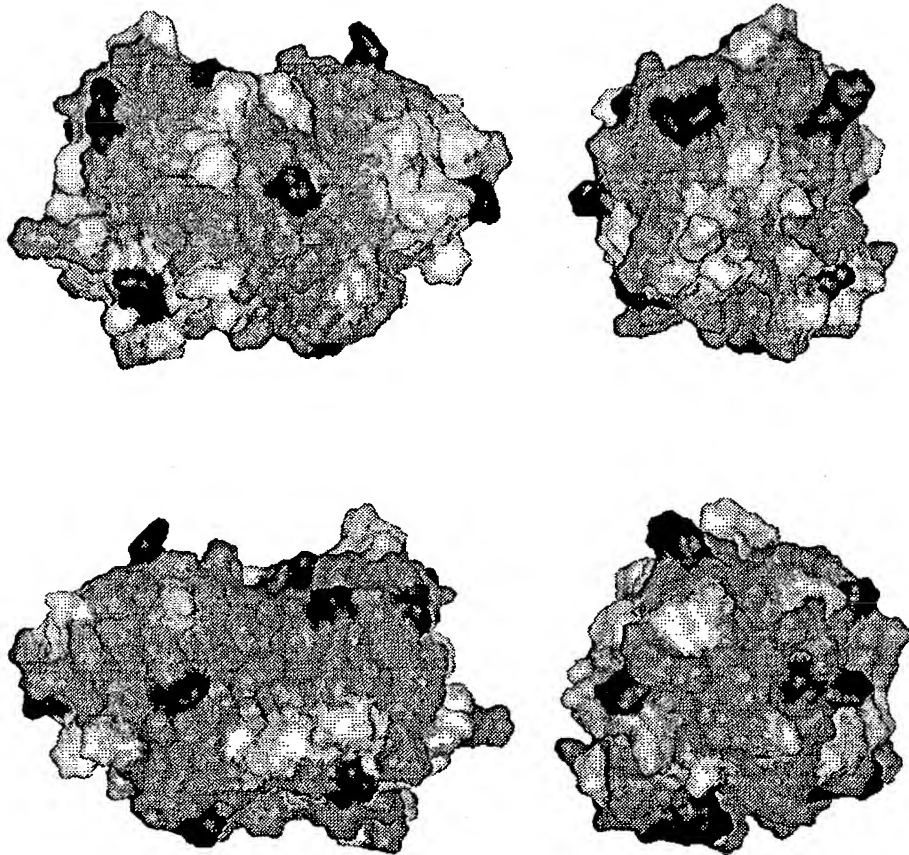
FIG. 36



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FIG. 37



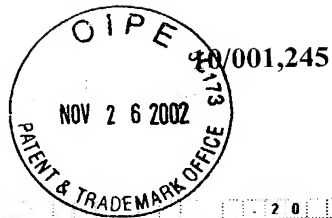
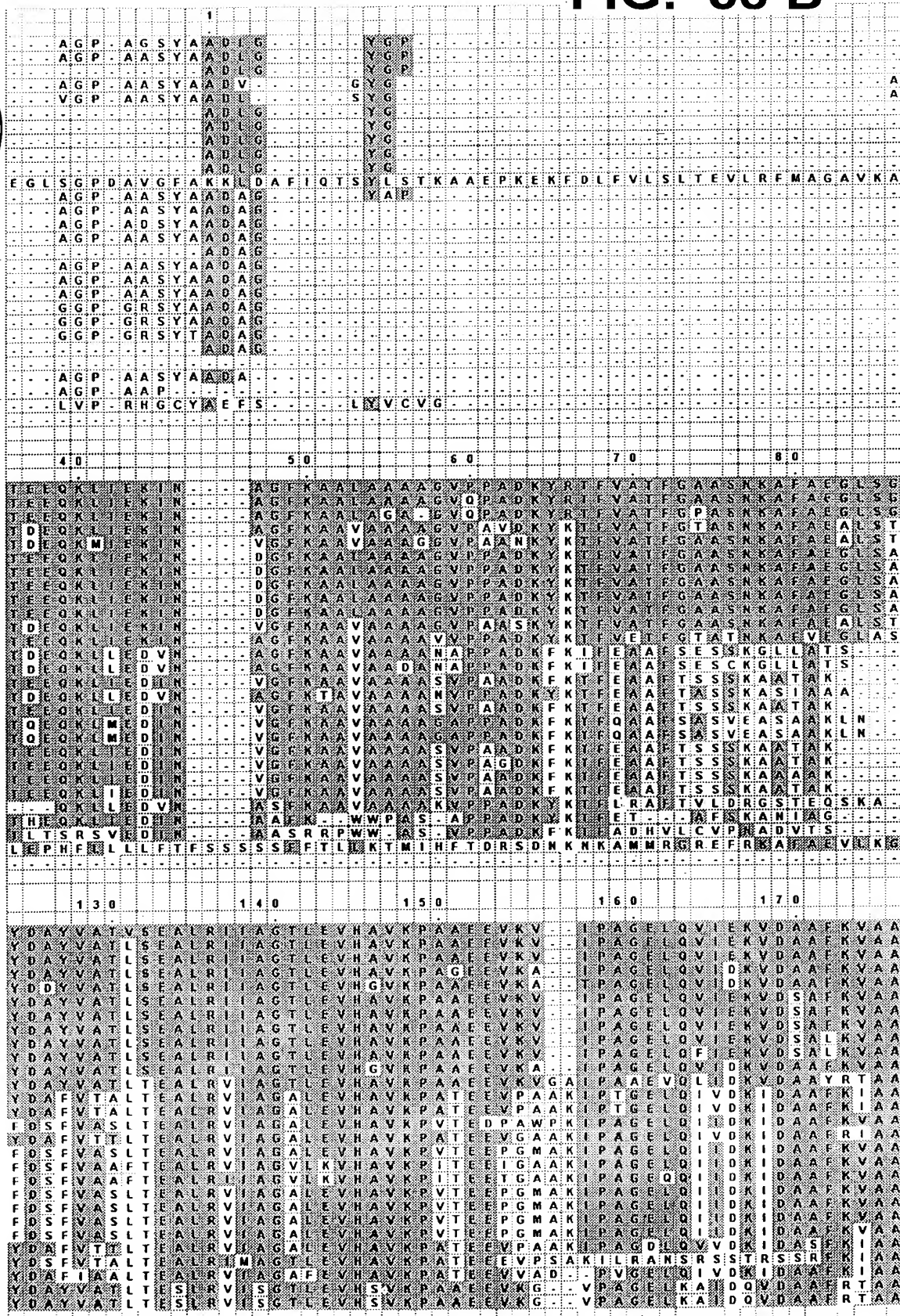


FIG. 38 A

		2 0	1 0	
trj081341j081341	Phi p 5.0103		MAVHQYTVALLFLAVLV	
trj040960j040960	Phi p 5		MAVHQYTVALLFLAVLV	
spj040962jMP5A_PHLPR	Phi p 5 A		MAVHQYTVALLFLAVLV	
spjP22265jMP92_POAPR	Poa p 5 (KBG41)		MAVHQYTVALLFLAVLV	
spjP22266jMP93_POAPR	Poa p 5 (KBG60)		MAVQKYTVALLFLAVLV	
trj065319j065319	Phi p 5			
trj065320j065320	Phi p 5			
trj065321j065321	Phi p 5			
trj065318j065318	Phi p 5			
trjP93467jP93467	Phi p 5			
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)		MDKANGAYKTALKAASAVAPAEKFPVFQATFDKNLK	
spj040237jMP5B_LOLPR	Lol p 5B		MAVQKHTVALFLAVLV	
trj09XF24j09XF24	Lol p 5A		MAVQKYTVALLFLAVLV	
trj09SC99j09SC99	Lol p 5C		MAVQKYTVALLFLAVLV	
trj081343j081343	Phi p 5.0206		MAVQKYTVALLFLAVLV	
trj023972j023972	Hol 15			
trj081344j081344	Phi p 5.0207		MAVQKYTVALLFLAVLV	
trjAAG42255jAAG42255	Hol 15B		MAVQKYTVALLFLAVLV	
trjAAG42254jAAG42254	Poa p 5		MAVQKYTVALLFLAVLV	
trj081342j081342	Phi p 5.0203		SVKRSNGSAEVHRGAVPRRGPR	
trjP93466jP93466	Phi p 5		AVPRRGPR	
spj040963jMP5B_PHLPR	Phi p 5B		AAAVPRRGPR	
trj09SBE0j09SBE0	Phi p 5.0204			
trj023971j023971	Phi p 5.02			
spjP56166jMP53_PHAHQ	Phi a 5.3		MAVQKYTVALLFLAVLV	
HAHQ	Phi a 5.1		MAVQKYTVALLFLAVLV	
trj004828j004828	Hor v 9		MAHSGREHS AVPRRRNLVA	
trjQ39995jQ39995	Hor v 5 (30kDa)			
		1 0	2 0	3 0
trj081341j081341	Phi p 5.0103		ATPAAAPAGYTTATPAAAPAG	
trj040960j040960	Phi p 5		ATPAAAPAGYTTATPAAAPAG	
spj040962jMP5A_PHLPR	Phi p 5 A		ATPAAAPAGYTTATPAAAPAG	
spjP22265jMP92_POAPR	Poa p 5 (KBG41)		PATLAPATPAAAPAGYTTATPAAAPAG	
spjP22266jMP93_POAPR	Poa p 5 (KBG60)		PATLAPATPAAAPAGYTTATPAAAPAG	
trj065319j065319	Phi p 5		GPATPAAAPAG	
trj065320j065320	Phi p 5		GPATPAAAPAG	
trj065321j065321	Phi p 5		GPATPAAAPAG	
trj065318j065318	Phi p 5		GPATPAAAPAG	
trjP93467jP93467	Phi p 5		GPATPAAAPAG	
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)		P P A S K F P A K P A P K V A A Y T P A A P A G	
spj040237jMP5B_LOLPR	Lol p 5B		ATPATPAAAPATAATPATPATPATPAA	
trj09XF24j09XF24	Lol p 5A		YTPAAAATPATPAA	
trj09SC99j09SC99	Lol p 5C		YTPAAAATPATPAA	
trj081343j081343	Phi p 5.0206		YAPATPAAAG	
trj023972j023972	Hol 15		YAPATPAAAG	
trj081344j081344	Phi p 5.0207		YAPATPAAAG	
trjAAG42255jAAG42255	Hol 15B		YAPATPAAAG	
trjAAG42254jAAG42254	Poa p 5		YAPATPAAAG	
trj081342j081342	Phi p 5.0203		YAPATPAAAG	
trjP93466jP93466	Phi p 5		YAPATPAAAG	
spj040963jMP5B_PHLPR	Phi p 5B		YAPATPAAAG	
trj09SBE0j09SBE0	Phi p 5.0204		YAPATPAAAG	
trj023971j023971	Phi p 5.02		YAPATPAAAG	
spjP56166jMP53_PHAHQ	Phi a 5.3		GPATPAAAPAG	
HAHQ	Phi a 5.1		GPATPAAAPAG	
trj004828j004828	Hor v 9		GPATPAAAPAG	
trjQ39995jQ39995	Hor v 5 (30kDa)		GPATPAAAPAG	
		9 0	1 0 0	1 1 0
trj081341j081341	Phi p 5.0103		EPKKG	
trj040960j040960	Phi p 5		EPKKG	
spj040962jMP5A_PHLPR	Phi p 5 A		EPKKG	
spjP22265jMP92_POAPR	Poa p 5 (KBG41)		EPKKG	
spjP22266jMP93_POAPR	Poa p 5 (KBG60)		EPKKG	
trj065319j065319	Phi p 5		EPKKG	
trj065320j065320	Phi p 5		EPKKG	
trj065321j065321	Phi p 5		EPKKG	
trj065318j065318	Phi p 5		EPKKG	
trjP93467jP93467	Phi p 5		EPKKG	
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)		EPKKG	
spj040237jMP5B_LOLPR	Lol p 5B		EPKKG	
trj09XF24j09XF24	Lol p 5A		EPKKG	
trj09SC99j09SC99	Lol p 5C		EPKKG	
trj081343j081343	Phi p 5.0206		EPKKG	
trj023972j023972	Hol 15		EPKKG	
trj081344j081344	Phi p 5.0207		EPKKG	
trjAAG42255jAAG42255	Hol 15B		EPKKG	
trjAAG42254jAAG42254	Poa p 5		EPKKG	
trj081342j081342	Phi p 5.0203		EPKKG	
trjP93466jP93466	Phi p 5		EPKKG	
spj040963jMP5B_PHLPR	Phi p 5B		EPKKG	
trj09SBE0j09SBE0	Phi p 5.0204		EPKKG	
trj023971j023971	Phi p 5.02		EPKKG	
spjP56166jMP53_PHAHQ	Phi a 5.3		EPKKG	
HAHQ	Phi a 5.1		EPKKG	
trj004828j004828	Hor v 9		EPKKG	
trjQ39995jQ39995	Hor v 5 (30kDa)		EPKKG	
		1 0 0	1 1 0	1 2 0
trj081341j081341	Phi p 5.0103		EPKKG	
trj040960j040960	Phi p 5		EPKKG	
spj040962jMP5A_PHLPR	Phi p 5 A		EPKKG	
spjP22265jMP92_POAPR	Poa p 5 (KBG41)		EPKKG	
spjP22266jMP93_POAPR	Poa p 5 (KBG60)		EPKKG	
trj065319j065319	Phi p 5		EPKKG	
trj065320j065320	Phi p 5		EPKKG	
trj065321j065321	Phi p 5		EPKKG	
trj065318j065318	Phi p 5		EPKKG	
trjP93467jP93467	Phi p 5		EPKKG	
spjP22264jMP91_POAPR	Poa p 5 (KBG 31)		EPKKG	
spj040237jMP5B_LOLPR	Lol p 5B		EPKKG	
trj09XF24j09XF24	Lol p 5A		EPKKG	
trj09SC99j09SC99	Lol p 5C		EPKKG	
trj081343j081343	Phi p 5.0206		EPKKG	
trj023972j023972	Hol 15		EPKKG	
trj081344j081344	Phi p 5.0207		EPKKG	
trjAAG42255jAAG42255	Hol 15B		EPKKG	
trjAAG42254jAAG42254	Poa p 5		EPKKG	
trj081342j081342	Phi p 5.0203		EPKKG	
trjP93466jP93466	Phi p 5		EPKKG	
spj040963jMP5B_PHLPR	Phi p 5B		EPKKG	
trj09SBE0j09SBE0	Phi p 5.0204		EPKKG	
trj023971j023971	Phi p 5.02		EPKKG	
spjP56166jMP53_PHAHQ	Phi a 5.3		EPKKG	
HAHQ	Phi a 5.1		EPKKG	
trj004828j004828	Hor v 9		EPKKG	
trjQ39995jQ39995	Hor v 5 (30kDa)		EPKKG	

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FIG. 38 B



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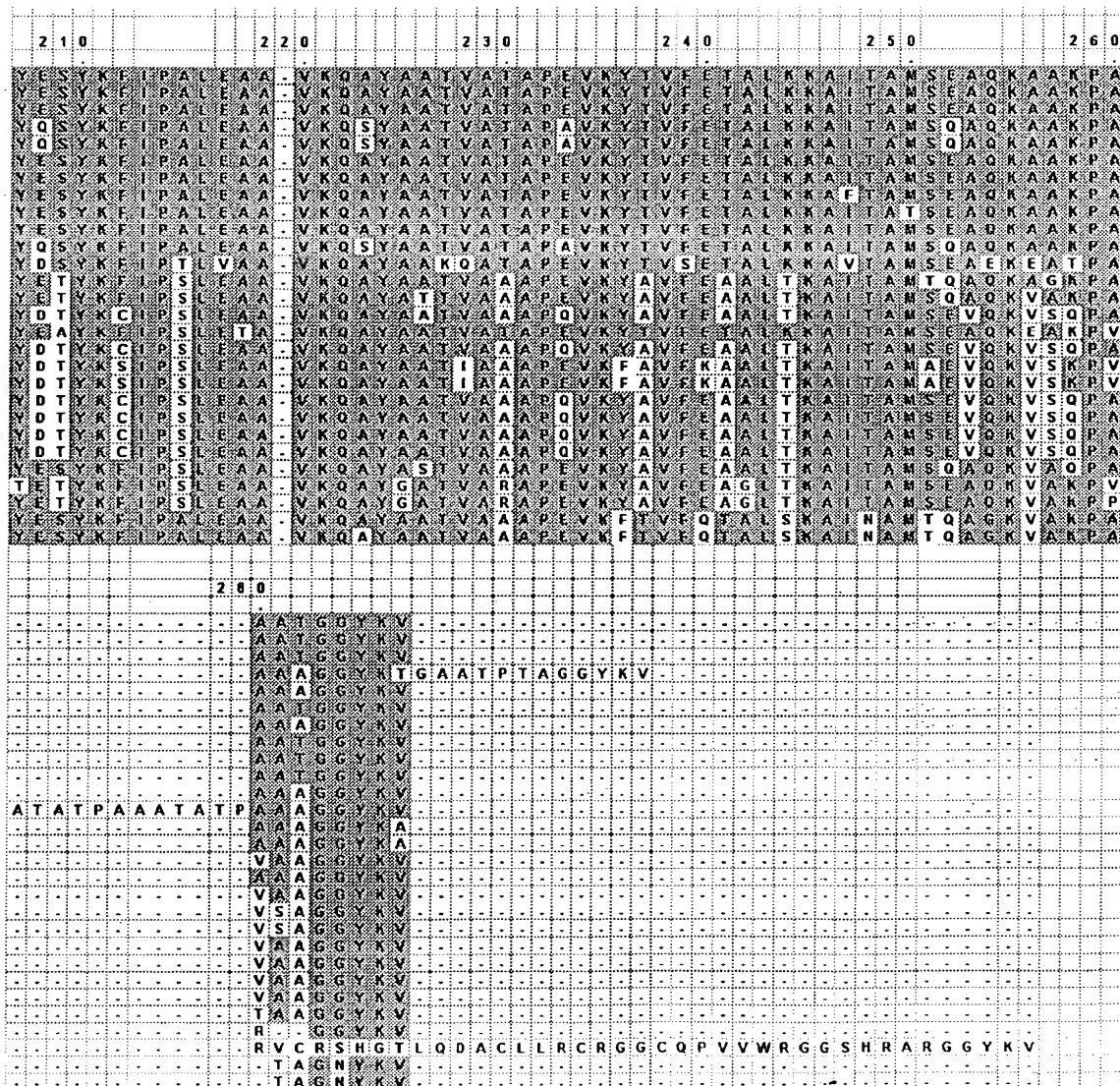
FIG. 38 C

										1 0 0										1 9 0										2 0 0									
tr081341 081341	Phl p 5.0103	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr040960 040960	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp040962 MP5A_PHLPR	Phl p 5 A	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp022285 MP92_POAPR	Poa p 5 (KBG41)	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp022286 MP93_POAPR	Poa p 5 (KBG60)	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr065319 065319	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr065320 065320	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr065321 065321	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr065318 065318	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr093467 093467	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp022284 MP91_POAPR	Poa p 5 (KBG 31)	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp040237 MP5B_LOLPR	Lol p 5B	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr09XF24 09XF24	Lol p 5A	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr09SC99 09SC99	Lol p 5C	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr081343 081343	Phl p 5.0206	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr023972 023972	Hol 15	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr081344 081344	Phl p 5.0207	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr081344 081344	Hol 15B	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr081344 081344	Hol 15B	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr081342 081342	Phl p 5.0203	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr093466 093466	Phl p 5	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp040963 MP5B_PHLPR	Phl p 5B	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr09SBE0 09SBE0	Phl p 5.0204	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr023971 023971	Phl p 5.02	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
sp056166 MP53_PHAHQ	Pha a 5.3	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
HAAQ	Pha a 5.1	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr004828 004828	Hor v 9	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
tr039995 039995	Hor v 5 (30kDa)	-	-	-	-	-	-	-	-	T	A	A	A	A	P	A	N	D	K	F	T	V	F	E	A	A	F	N	D	A	I	K	A	S	T	G	G	A	
2 7 0																																							
tr081341 081341	Phl p 5.0103	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr040960 040960	Phl p 5	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040962 MP5A_PHLPR	Phl p 5 A	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp022285 MP92_POAPR	Poa p 5 (KBG41)	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp022286 MP93_POAPR	Poa p 5 (KBG60)	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065319 065319	Phl p 5	T	E	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065320 065320	Phl p 5	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065321 065321	Phl p 5	T	E	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr065318 065318	Phl p 5	T	E	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr093467 093467	Phl p 5	T	E	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp022284 MP91_POAPR	Poa p 5 (KBG 31)	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040237 MP5B_LOLPR	Lol p 5B	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr09XF24 09XF24	Lol p 5A	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr09SC99 09SC99	Lol p 5C	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081343 081343	Phl p 5.0206	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr023972 023972	Hol 15	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081344 081344	Phl p 5.0207	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081344 081344	Hol 15B	A	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081344 081344	Hol 15B	A	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr081342 081342	Phl p 5.0203	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr093466 093466	Phl p 5	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp040963 MP5B_PHLPR	Phl p 5B	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr09SBE0 09SBE0	Phl p 5.0204	T	G	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
tr023971 023971	Phl p 5.02	A	A	-	-	-	-	-	-	A	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
sp056166 MP53_PHAHQ	Pha a 5.3	R	L	S	P	Q	-	-	-	P	Q	V	L	P	L	A	A	G	G	A	A	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
HAAQ	Pha a 5.1	L	S	P	Q	-																																	

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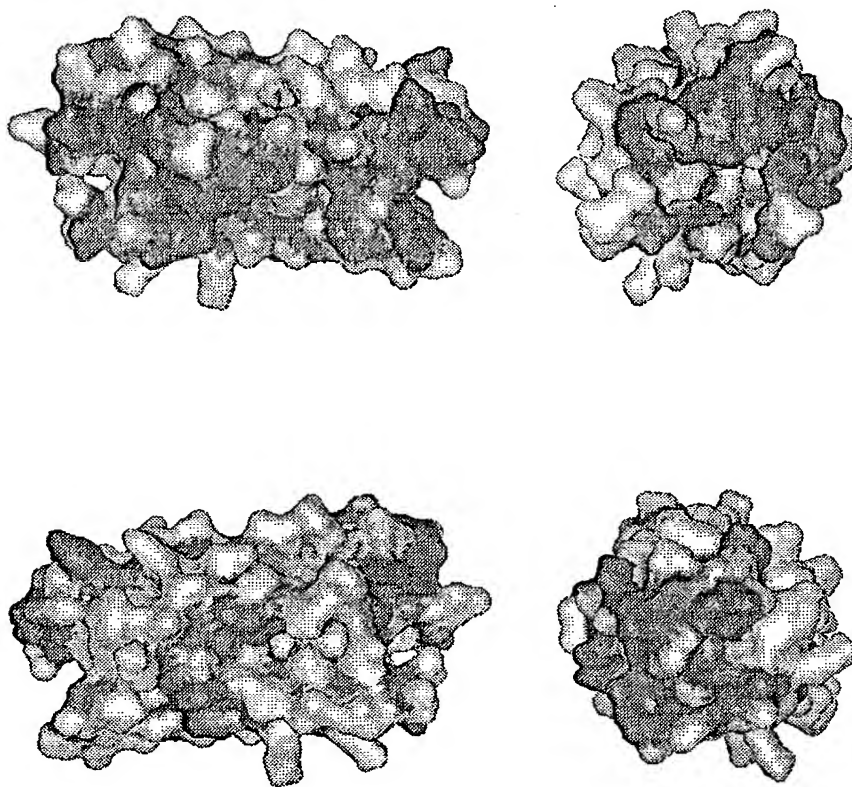
FIG. 38 D



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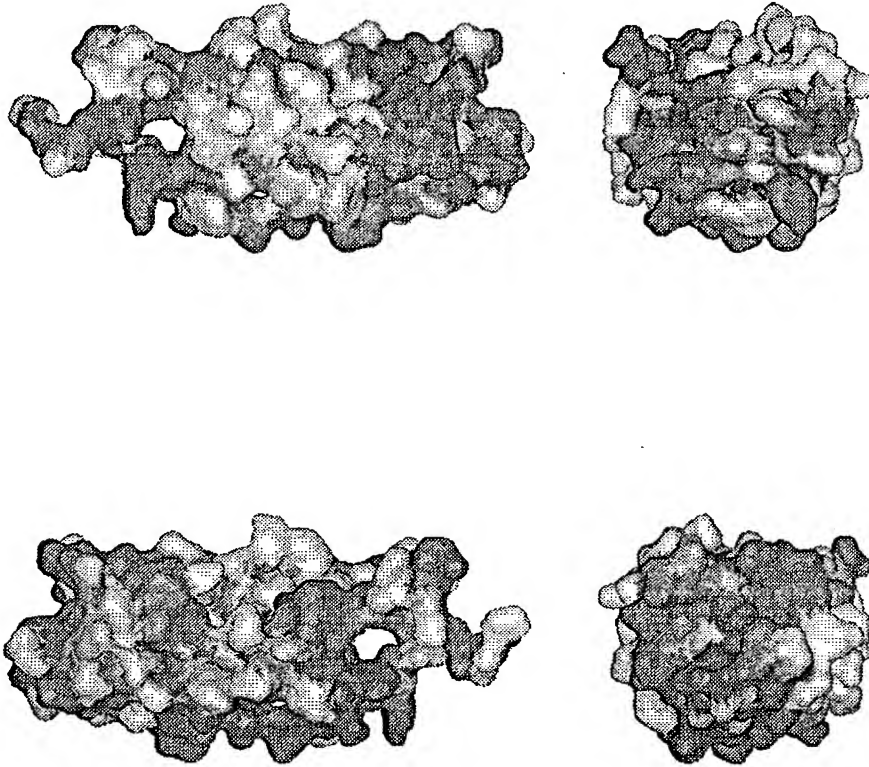
FIG. 39 A



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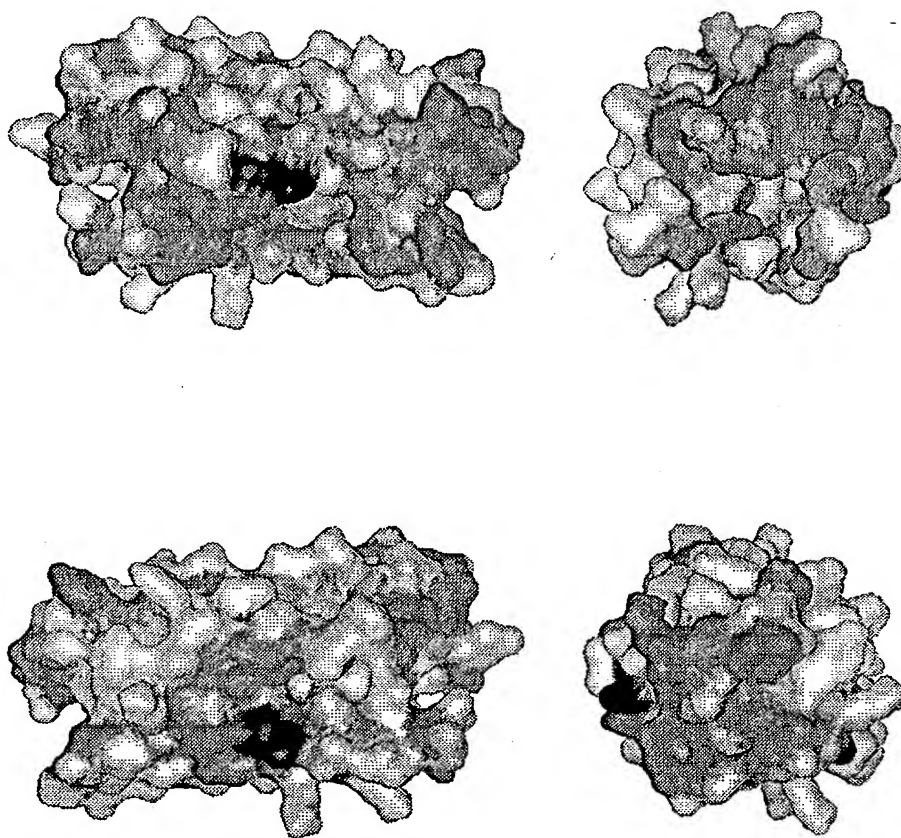
FIG. 39 B



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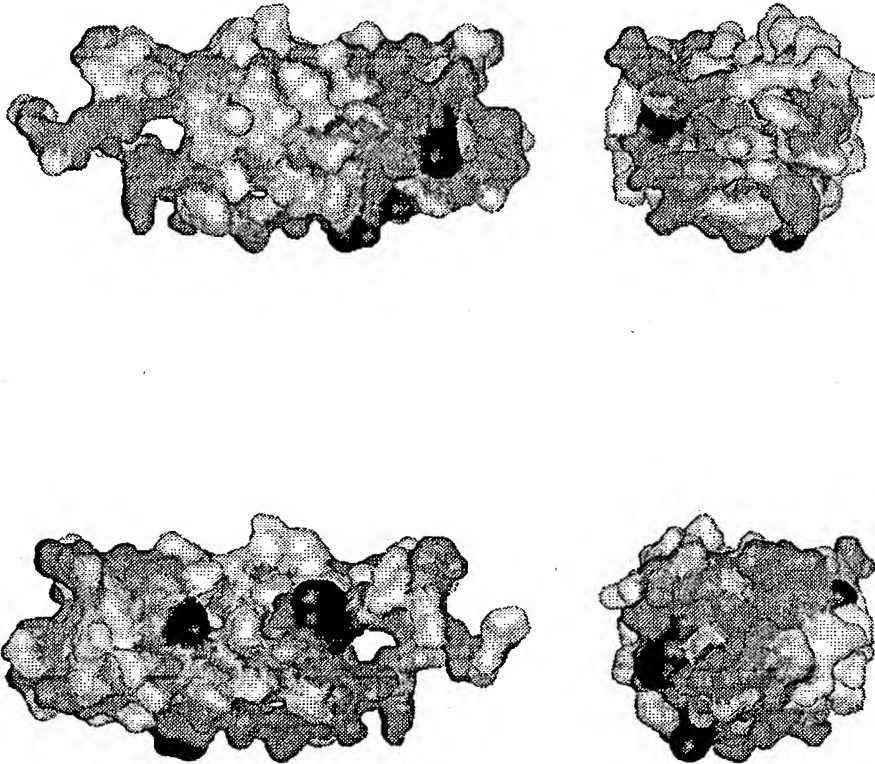
FIG. 40 A



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FIG. 40 B



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FIG. 41

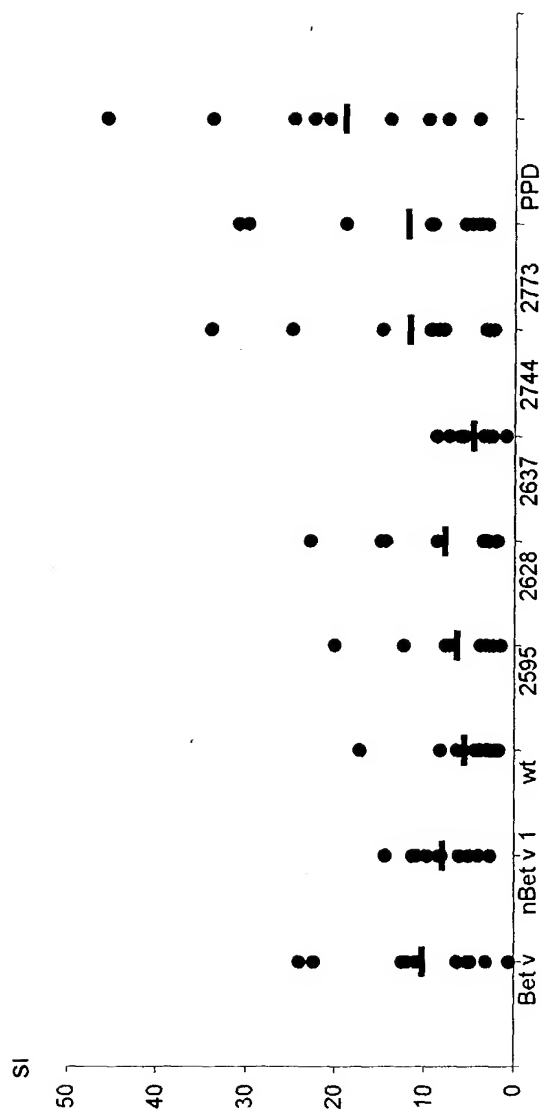
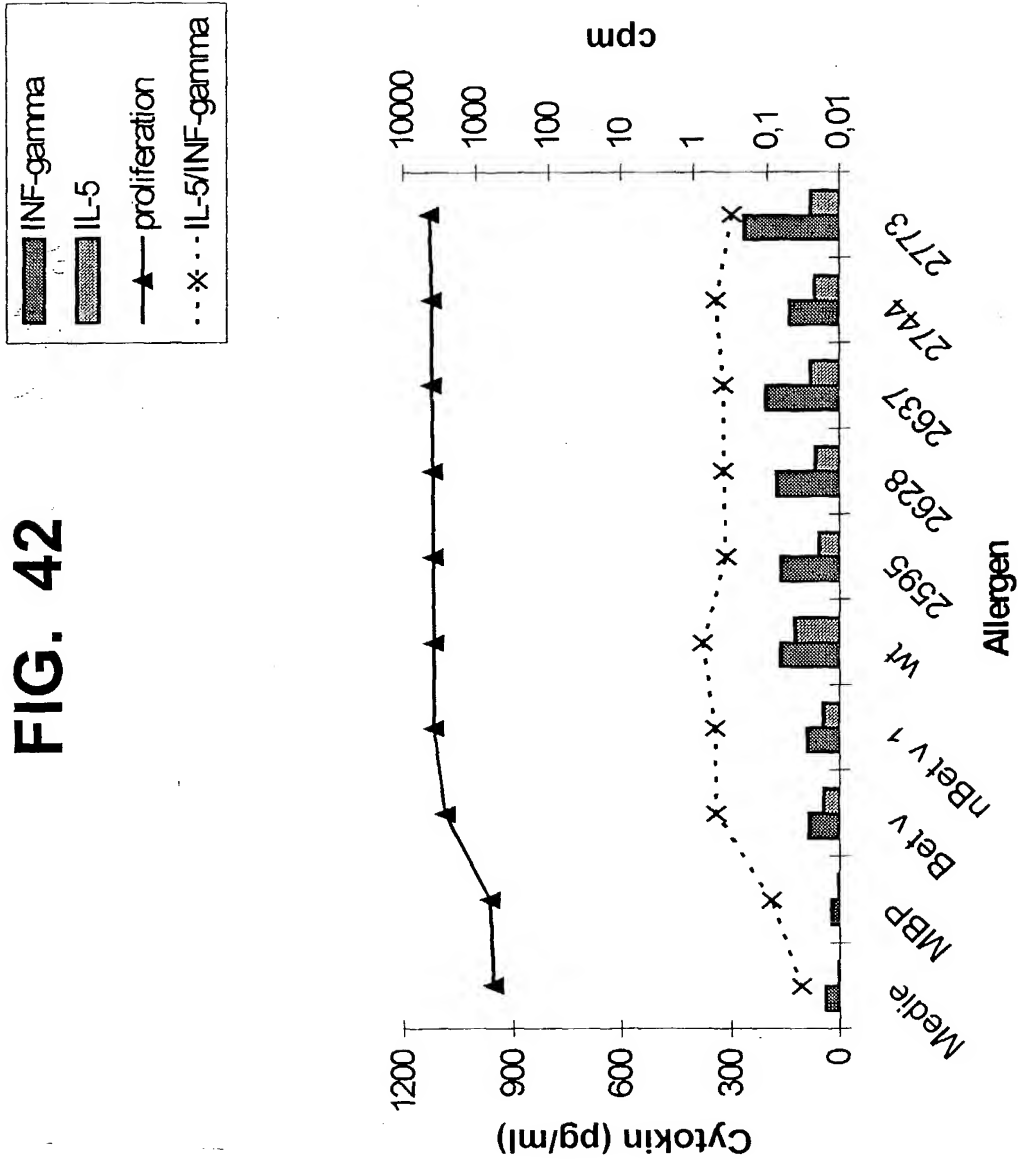




FIG. 42



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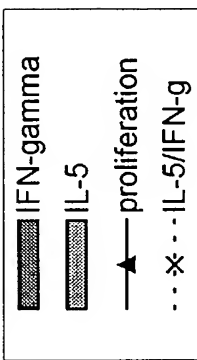
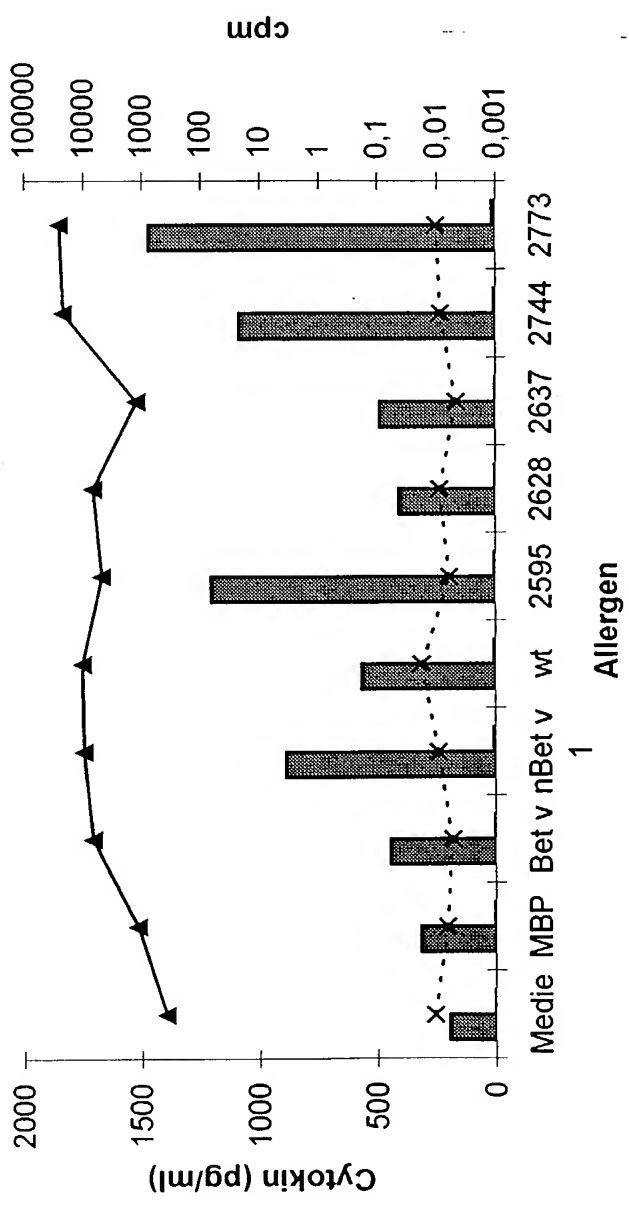


FIG. 43





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FIG. 44

